Access DB# 195

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: David Fox Examiner #: 6540 Date: 5/12/04
Requester's Full Name: 1/4 V Examiner #: Date:
Art Unit: 1638 Phone Number 30 20795 Serial Number: 09/7023 Mail Box and Bldg/Room Location: REM 2 69 Results Format Preferred (circle): PAPER DISK E-MAIL
26 18
If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.
Title of Invention:
Inventors (please provide full names):
Earliest Priority Filing Date: 3/9 9
For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.
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please search renewed SEQ 10 NO: 2
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STAFF USE ONLY	Type of Search	Vendors and cost where applicable
Searcher: APNO/d	NA Sequence (#)	STN
Searcher Phone #: 2-255	AA Sequence (#)	Dialog
Searcher Location:	Structure (#)	Questel/Orbit
Date Searcher Picked Up: 5/3/0 4	Bibliographie	Dr.Link
Date Completed: 5/17/04	Litigation	Lexis/Nexis
Searcher Prep & Review Time:	Fulltext	Sequence Systems
Clerical Prep Time:	Patent Family	WWW/Internet
Online Time:	Other	Other (specify)



GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

cleic - nucleic search, using sw model ä

May 16, 2004, 10:21:20 ; Search time 2969 Seconds (withbot alignments) 3956.201 Million cell updates/sec 3956.201 Million cell updates/sec US-09-701-023-2 271

1 gtagcatcgatctctaacaa......ctactcatgagctctcttca 271 IDENTITY_NUC Gapop 10.0 , Gapext 1.0 ct score: ng table:

3470272 seqs, 21671516995 residues

ped:

number of hits satisfying chosen parameters: num DB seg length: 0 num DB seg length: 200000000

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processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Prod. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

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ALIGNMENTS

LATE

AF146794 linear PLA Arabidopsis thaliana NOZZLE (NZZ) gene, complete cds. AF14670 linear

PLN 29-SEP-1999

AF146794.1 GI:5007008

RESULT 1
AF146794
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS

SOURCE ORGANISM

Arabidopsis thallana (thele crees)
Arabidopsis thallana
BiArapidopsis thallana, Ereptophyta, Embryophyta, Tracheophyta,
BiArapidopsis, Viridiplantes; Streptophyta, Embryophyta, Tracheophyta,
Bornatophyta, Magnoliophyta, endicotyledons; core endicots,
rosida entosida II; Brassicales; Brassicacese; Arabidopsis.
1 (bases 1 to 113)
Schlesfindary, J. Blassubramanian, S., Sieber, P., Chevalier, D.,
Misman, R. and Schnaftz, N.

REFERENCE AUTHORS

Permatophyta; Magnoliophyta; endicotylpidons; orde eudicots; reacheophyta; pendicots; corde eudicots; corde eu

Arabidopsis thaliana (thale cress) Arabidopsis thaliana Enkaryoca' Viridiplana Streptophyta; Embryophyta; Tracheophyta;

ORGANISM

KEYWORDS

VERSION SOURCE REFERENCE AUTHORS TITLE

JOURNAL MEDLINE PUBMED

AF159255.1 GI:5566239

"Chang, H. C., Ye, D., Xu, J. and Sundaresan, V.
Direc Submission.
 Bubmitted (H.-UWL-1999) Plant Molecular Genetics, Institute of
Nolecular Agrobiology, 1 Research Link, Singapore Location/Gealifiers

/organism="Arabidopsis thaliana"

1. .1302

SOLITOR

FEATURES

TITLE

REFERENCE AUTHORS

/mol_type="mRNA" /cultivar="Landsherg erecta"

'db xref="taxon:3702"

/map="PG11-mi123" /note="nucleus" /chromosome="4"

'gene="SPL" 'gene="SPL"

. 1302

gene

SGO

Molecular analysis of MOZZLE, a gene involved in pattern formation and early sporogenesis duting sex organ development in Arabidopsis and early sporogenesis duting sex organ development in Arabidopsis proc. Natl. Acad. Sci. U.S.A. 96 (20), 11664-11669 (1999) 9942250 (1990) 99	tali		/product-work2126* /gene=wgw-work216* /gene=wgw-wgw-wgw-wgw-wgw-wgw-wgw-wgw-wgw-wgw	~~ x r r z x e	/gene="Kize" for paralidopsis thaliana Columbia ecotype gequence presented in GenBank Accession number AL030978" (76)2 "*Kize" for paralidopsis thaliana Columbia ecotype for a for paralidopsis thaliana Columbia ecotype for the formation of Generalidopsis Columbia ecotype for the formation of Generalization of Generalizat	dlarit Conse
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KBYEFFPGKYGERVSVVATTSSLVGDCSPNTIDLSLKL"
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470 TOGGSTCAGSTRATGAGACCCGCCCCC 529
470 TOGGSTCAGSTRATGAGACCTCCCCCC 529
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Marabidopsis thaliana

Bukaryotosis thaliana

Bukaryotosis (Midaliana)

Rarabidopsis (Midaliana)
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                                                                      Length 1302;
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                                                                      Score 127.4; DB 8;
Pred. No. 7.8e-32;
0; Mismatches 1;
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Arabidopsis thaliana sporocyteless (SPL) mRNA, complete cds.
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/note="MADS-box related protein"

/codon_start=1

/product="sporocyteless" /protein_id="AAD45344.1" /db_xref="G1:5566240"

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RAKALCKOOLWARAKIVVUSELDVIDDLE SPAADFGASAERSKVGRYDLCKRKOR
BRAKTDGITAKQA PEPPELTRAGISGITULAKERDILAKIVTKGKSKOLASGOSSET
GOBGRAQAAMEMPIQFPQYMQNFQGHGYPPPYMFCWQGOGGPYFHGXMQWPVNKGDVE
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LVERINPSDFLLDIANGKPLLVISCWPSVGSDESQRPRAMKAALVAFYKTNLLDSVIN
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protein id="CAB43875.1"
db_xref="G1:4972068"
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37369. .38011,38273. .38386))
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product=putative protei"
protein id="CAB48871.1"
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/gene="F27G19.30"
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protein da-Cabajan. 1.4

(b. xref-al.1497268**) (b. xref-al.1497268**)

(b. xref-al.1497268**) (b. xref-al.1497268**)

(c. xref-al.1497268**) (b. xref-al.1497268**) (
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BERSKLUDWYLCZHIKKTSSEKORYATVYKOKEREKINGSSSSSSSQLDDVLOSP
PEI KODSPYLLPKWISLKTILKGRPWAGLACHPTPELAFTYGLFSVGKTAFRAADS
BABSGHVNRQQNSSGLTGSFCYSSGFOVSGQTFEFRQ*
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// Adome="17" at tandem repeat"
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                                                                                                                                                                             Bevan, M., Hilbert, H., Braun, M., Holzer, B., Brandt, A., Duestertheft, A., Bancroft, I., Mewes, H. W., Mayer, K. F. X., Lemcke, K., Manhaupt, G. and Schueller, C. Dipublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5126. .5143
Morbe-there is a mismatch in this homopolimeric stretch to the overlapping BAC M4122; 18(E27019) versus 17(M4122) A's; the genomic DNA clearly shows 18 A's"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Substitute (10-Mys. 1999) MTPS, at the Max-Dlanck-Institut feer Blochmie, and Alpherential Bea D-62152 Martineried FRG. B-mail: Schedlesmisc blochem mgg de Project Coordinator: Miss Reven, Nobelcular Generics Department, Cambridge Laboratory, John Innes Gentre, College Jane, MS 700 Norwich, US.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E-mail: michael. bevambherc ac uk
Information on performance of analysis and a more detailed
amocation of this entry and other sequences of chromosomes 3. 4
and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.
Location/Qualifiers
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/note="overlap to BAC W4122 ; please refer to this entry
for analysis and annotation"
                    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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complement(join(13517, .31960,32044, .32335,32394,
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Arabidopsis thaliana (thale cress) Arabidopsis thaliana GI:3269280

AL030978.1 AL030978 project)

DEFINITION

ATM4122/c ACCESSION VERSION

RESULT 4 LOCUS SOURCE ORGANISM

ATM4122 83371 bp DNA linear PLN 10-MAR-2000 Arabidopsis thaliana DNA chromosome 4, Pl clone M4122 TESSA

Zea mays,

contains EST gb:AW004308.1, AA712235, 235393" /codon_start=1

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Direct Submission with Park 2000 WIPS, at the Max-Planck-Institut fuer Submitted On-Max-2000 WIPS, at the Max-Planck-Institut fuer Biochemie, Am Knopferspitz 18 Ap 10-5125 Martinsted, RRG, E-mail: Hanckemips biochem.mgg de mayeramips biochem.mgg de the Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mgg.de/proj/thal/. Enkaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Sgarnatophyta, Magnoliophyta, eudicotyledons, one eudicots, rosaida, eutrosida II, Brassicales, Brassicaceae, Atabidopsis. 'note="similarity to retrotransposon Opie-2, Zea mays, oin(3583. 3719,3767. 4131,4357. 4828,4949. 7931) Gene="AT4g27210" note="similarity to Hopscotch retrotransposon, PID:g1657769 contains EST gb:T46634, AA404771, A1997526.1" join(737. .1811,1828. .2002,2037. .3246) /gene="AT4g27200" 'organism="Arabidopsis thaliana" /product="putative protein" /protein_id="CAA19714.1" /db_xref="GI:3269281" /mol_type="genomic_DNA" /variety="Columbia" /db_xref="taxon:3702" /chromosome="4" EKAFNIKLENRFLTLDSEIPA" Location/Qualifiers /37. .3246 /gene="AT4g27200" 737. .1811 /gene="AT4g27200" 1812. .1827 /gene="AT4g27200" 828. .2002 gene="AT4g27200" 1003. .2036 'gene="AT4g27200" 2037. .3246 'gene="AT4g27200" 'gene="AT4g27200" 1583. .7931 'gene="AT4g27210" 'codon_start=1 2973. .3217 number=3 number=1 number=1 number=2 number=2 1. .83371 (bases 1 to 1) source intron intron AUTHORS LTR gene exon EFERENCE JOURNAL exon exon gene SG E E PEATURES COMMENT

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proteases active sites AA449-459" /codon_start=1 product="putative protein" protein_ld="CAA19716.1" db_xref="GI:326283" db_xref="GOA:081825"

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ALABIGOS. 01:7269538 /dd_xtef="goalogisge" /dd_xtef="sptembl.ogisges" /t_tagist.oid = WaggrqqJsggaakksttsrsskagiqppvgriarelkngkyaer vgagapytaanytg:taartbelagnaardnkktrivppppigiavrhdbeelskilgdd 132 GOGCIACAAGGCTTCCCAAGCTCA-TCGGGAGCAACAGGATCTATTGTGGTGGAGTCGGG 190 191 TCGGGTCAGGTTATGATCGACCCGGTTATTTCTCCATGGGGTTTTGTTGAGACCTCCTCC 1; Gaps /hote="strong similarity to histone H2A.4, Triticum assixum, PRE:SS2512 CODIFICATION HISTONE H2A SIGNATURE AA23-29 contains EST gb:AI995882.1, T04821, T43418" DB 8; Length 83371; 13524. .14334 /gene="XA497730" complement(join(13524. .13730,14146. .14334)) /gene="RT4927230" complement [join(13524. .13730,14146. .14334)) /gene="AT4g27230" Indels /codon_start=1 /product==histone H2A-like protein" /protein_id="CAA19717.1" /db_xref="G1:3269284" 1, 16169. .17649 /gene="AT4g27240" join(16169. .16829,17015. .17649) TIANGGWAPNIHNLLLPKKAGSSKPTEED" complement (13524. .13730) /gene="AT4g27230" 47.0%; Score 127.4; DB 98.6%; Pred. No. 1e-31; Live 0; Mismatches complement (13731, .14145) /gene="AT4g27230" /number=1 complement (14146. .14334) /gene="AT4g27230" Arabidopsis thaliana (thale cress) Arabidopsis thaliana complement (9962, .12721) /gene="AT4927220" 59018 ACTACTCATGAGCTCTCTTCA 58998 251 ACTACTCATGAGCTCTTCA 271 /number=1 /number=1 Matches 139; Conservative Query Match Best Local Similarity VERSION KEYWORDS SOURCE ORGANISM ATCHRIV66/c intron DEFINITION exon gene ACCESSION gene gene exon CDS RESULT 5 쉺 à 셤

/number-2 complement (7485, 7689) /gene=781424866	/// //////////////////////////////////	Complement (7764. 7851) complement (7764. 7851) /yiene=*Af4926860"	t (7852. 4g26860		complement (80038080) /gene=*AT4g26860" /number=8	complement (80818147) /gene="AT4g26860"	/ Juubber	/ number = 5 Complement (83278548)	/ yelle= 41.92.0000- /number=7 92.86 . 11474	/gene="AT4g26870" join(92369715,97839893,999610079,1019110481,	1055510665,1087411069,1115611270,1134811474) /gene="AT4g26870"	<pre>/note="similarity to aspartate-tRNA ligase (EC 6.1.1.12) -Methanobacterium thermoautotrophicum, GB:AE000809</pre>	Contains Aminoacyl-transfer RNA synthetases class-II signatures AA293-311,Aminoacyl-transfer RNA synthetases	Contains Est gb:234062, AA720362"	/codor_start=1 /product=1utative aspartate-tRNA ligase" /octsia id=exposed 1"	/procein_id="AB/9942.1" /Ab xref="G1726940"	/dd_xref="GOA:U95&1" /db_xref="STREMBL:095%27" /translation="WVGSBVLEECGEKISKXESKKRAAKLEXILRKOERPEATSSSLS	LEEEDESCSSNYGDVTTNELOSAVECKELTDVSNIJVEETVGSEVSTRGRLHKORELVGT KLPVIIREGGFTVOCVVEETRVGANMIKPVKOLSRESVVELIGVVSHPRKPIJGGTTOO	VEIHVRIOMYCLSRSLIPNLPLVVEDAARSBSDIEKSGKOTALNMRYLDIRTPANGALFR IQCQVQIAPREYLQSKGFLEIHTPKLIAGSSEGSAVFRLDYKGQPACLAQSPQLHKQ	MAICGDMRRVFEVGPVFRAEDSFTHRHLCEFVGLDVEMEIRMHYSEIMDLVGELFPPI FTKIEBRCPKELESVRKOYPPOSLKEAGBEVDPLGDLNTSSERKLGOLVLEKYKTEFY	MLHRYPSAVRPFYTMPYENDSNYSNSFDVFIRGEBIMSGAORIHDPELLEKRARECGI DVKTISTYIDAFRYGAPPHGGFGVGLERVVMLLCALNNIRKTSLFPRDSQRLTP"	92369715 /gene="AT4926970"	/number=1 9716978 /gene="A7426870"	/number=1 97839893	/gene="#I44g26B70" /number=	98949995 /gene="AT4g26870"	/number=2 999610079	/gembe=*A14g2b8/0* /rumbe=*3 1008010190	/gene-13/4926870* /number-3 1019110481
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Engglaaprelfarlkardpoledduttyfgddaclpniwytnespegffiogralgyddo
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    Ghadzesen V., Martienssen, R., O'Shaughnessy, A., May, B., Burdaresen, V., Martienssen, R. and McCembie, M.R.
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LOTAWITESCHAEL, Institut fuer Porstgeneth und 
Forstpfalmschuckung, Sieker Jandstrasse 2, Grosshansdorf 22927,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 AGCATCGATCTCTAACAACGCTACCCGTTTACCCGTACCCGGTAGACCCGGGTGTTGTGCT 62
                                                                                                                                                                                                                                                                                                                                                                                                                              118 AGAGTCCTTCATTGACGATCTTCTTCATATCGTCTTTTCGTTTCACCGATTTGTTCTTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 CTAGGGATGAAACGGTCGGTAACGGTCGGTAAAATACGGGCNACANTTTCTAANNAT 1
                                                                                                                                                                                                                                                                                0; Gaps
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                                                                                                                                                                                             Length 414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="transgenic line Esch5:35S-Ac-rolC#3"
                                                                                                                                                                                                                                                                          48; Indels
                                                                                                                                                                                             Score 43.6; DB 8;
Pred. No. 0.0025;
0; Mismatches 48;
/db xref="taxon:3702"
/ecotype="Landsberg"
/note="transgenic line GT6240"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <1. .112
/transposon="Ac element"
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/cultivar="Esch5"
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/mol type="genomic DNA"
/db_xref="taxon:4577"
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1. .208
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/transgenic
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1 Similarity 59.3%;
70; Conservative
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gene CDS

TIAGIHGNYTDMNSEEYQCAMIDWYRRVPDRVBAVVGBOVANFADFATSGGILRVGGN KKGIFTPDRKVFSAALLLQKRATONNFGEKPQQ5GKQ" complement (6381. .6414) /noce="CaNV 355 promoter -46 region" misc_feature

58 GIGCTACAGGGAIGAAAACGGTCGGTAACGGTCGGTAAAATACTACGGGATTTTTCCCAT 117 Gaps ö ry'March 15.2%; Score 41.2; DB 12; Length 6875; Le Local Similarity 74.3%; Pred, No. 0.019; ches 23; Conservative 0; Manatches 18; Indels 0;

gene

AF433043.1 GI:16903092 AF433043 NOILI SSION

circular SYN 11-NOV-2001 Cloning vector pWS32, complete sequence. AF433043 DNA 6928 bp

artificial sequences; vectors. 1 (bases 1 to 6928) Cloning vector pWS32 Cloning vector pWS32

ANISM

ENCE HORS 3

Sundarean, V. Stringer, P. Viope, T., Haward, S., Jones, J.D., Dean, C., Ma, H. and Martiensen, R. Sinjant development revealed by enhancer betterns of gene action in julant development revealed by enhancer trap and gene trap transposable elements Genes Dev. 9 (14), 1797-1810 (1995)

7622040 RNAL

2 (bases 1 to 6928)
de la Bastide, N. Beston, R., O'Shaughnessy, A., May, B.,
Bastide, W., Martienssen, R. and McCombis, M.R.
Direct Submission of Submission of Submission of Submission of Spring Harbor Laboratory, 1 Bungtown
Rd, Cold Spring Harbor, NY 11784, USA

THORS

JRNAL,

organism="Cloning vector pWS32" /mol_type="other DNA"
/db_xref="taxon:176660" 1. .6928

source

64. ...1852 /organism="Cloning vector pWS32" | Mnol.type="chber DNA" | Ab zref="taxon:176660" | fransposon="Ds transposable element" | /note="S' fragment" 6511. .6702

source

/tränsposon="Ds transposable element" /note="3" fragment; transferred to TDNA vector pAJ8 for rensfermation of Arabidopsis thaliana" /organism="Cloning vector pWS32"
mol_type="other DNA"
db_xref="taxon:176660"

organism="Cloning vector pWS32"

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/training action - WORNDETPREITKLIDGEMERIDERRECHOWNERSLADGERS
/training-action - WORNDETPREITKLIDGEMERIDERRECHOWNERSLADGERS
INTROSPROCHO ADDI INTRAGENERIZIEREN OF THE PROTECTION OF THE PROTECT PULEVKTDESGALNELQDBAARLSKILATTGVPCAAVLDVVTBAGROMLLIGEVPGQDU. LSSHILAPAEKVSHAVARKALHUDARVGPRDAKARNI IRBKTRVRAGGAVDQDBLOB EHQOLAPAELFARLKARNPOEDLVVTHGDACLINIVNEKGRESGEFDCGRLGVADRY QDJALATROD ARELGGRANDRELVLYGIAAPDSQRIAPYRLLDEFF KELIARDKAHPSVVMKSIANEPDTREGGAREYFAPLAEATRKLIDFTPLTCVMVMFCD AHTDTTSOLFUVLLINEYTVOMYVOGODIATREKTLEKELIAMGEKLAPPTITSTVON TAHTDTSOLFUVLLINESTVOCAMLIDMYHKYPRVSAVVOEQVMYRADFATSQELIKVGGA /translation="MIEQDGLHAGSPAAWVERLFGYDWAQQTIGCSDAAVFRLSAQGR KKGI FTRDRKPKSAAFLLQKRWTGMNFGEKPQOGGKQ" Codom start=1 /transl_table=11 /product="neomycin phosphorransferase" /fprotein id='Ahi30402.1" /db.xref="Gi:16903093" /moi_type="other DNA" /baxref="texaon:176660" /transposon="18 transposable element" /note="3' fragment" /codon_start=1 /transl_table=11 /product="beta-glucuronidase" /protein_id="AAL30403.1" /db_xref="G1:16903094" complement (4550. .6361) complement (4550. .6361) 2376. .3170 /gene="npt2" 2376. .3170 /gene="npt2" /gene="uidA" 'gene="uidA"

complement (4364. .6615)
//note="synthetic GPA1 intron containing splice donors and acceptors in 3 reading frames"

intron

ORIGIN

58 GTGCTACAGGGATGAAAACGGTCGGTAACGGTCGGTAAATACTACGGGATTTTTCCCAT 117 Gaps ò 15.2%; Score 41.2; DB 12; Length 6928; 74.3%; Pred. No. 0.019; ive 0; Mismatches 18; Indels 0; Query Match Best Local Similarity 74.3 Matches 52; Conservative

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6857 TCATATTTAA 6848

AF355378/c

AP355378 San S772 bp DNA linear | Zea mays bz-m2(Ac) mutable allele, genomic sequence. AP355378 AF355378.1 GI:13898794 **Zea** mays 2еа шаув DEFINITION ORGANISM KEYWORDS

VERSION

SOURCE

PLN 01-MAY-2001

Enkaryott, viridiplatte, Structophtia Enhryophyta, Tracheophyta; Spannia Polici, viridiplatte, Structophtia Polici, Po

JOURNAL TITLE

AUTHORS

REFERENCE

11 11dy 1, 00.32.12

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AF51994

Programmer 197 bp DNA linear SYN 14-JUL-2002
Progulus tremula x Populus termuloidee transgent line
Beofis: 958-Ac-rol(#3 isolate SX414 with Zea may & celement, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="distal member of Dp26 duplication; carries a mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5887 TGGGCACTAGGGATGAAAACGGTCGGTAACGGTCGGTAAAATACCTCTACCGTTTTCATT 5828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 TGTGCTACAGGGATGAAAACGGTCGGTAAACGGTCGGTAAAATACTACGGGATTTTTCCCCA 116
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populus tremula x Populus tremuloides
Bukaryota, Viridiplantes; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kumarr S. and Piadúng, M.
Direct Simbission S. Bundesforschungsanstalt fuer Forst- und
Bolzwittechaft, Intelfut (Forstgreet's und
Bolzwittechaft, Intelfut (Forstgreet's und
Porepfilanzenzuechtung, Sieker Jandstrasse 2, Grosshansdorf 22927,
                                                                                                                                                                                                                                                                                                                                                       An-entable hybrid be alled produced by intragenic escophintion between the bz-mi mutent from Ez-HCC found in General Accession Numbers AF037598 and X07940 and the bz-s4 mutent from Ez-H2 with Minders AF037598 and X07940 and the Numbers AF0574 and X07937" and
                                                                                                                                                                                                                                                                                                                                'note="proximal member of Dp26 duplication; carries an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
roids; eurosids ; Malbighiales; Salicaceae; Saliceae; Populus.
I (Dasse: 1 to 197)
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                                                                                                                                                                                                                       /note="tandem duplication of bz locus
genotype: Bz(Dp26)-ml; Ac-mutable allele"
1. .6905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="target site direct repeat"
1316. .5880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="target site direct repeat"
5906. .6911
                                                                                                                                                                                                              'map="9S; between stkl and stc1"
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Plant Mol. Biol. (2002) In press
2 (bases 1 to 197)
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                                                                                                                                                  /db_xref="taxon:4577"
/chromosome="9"
                                                                'organism="Zea mays"
         Location/Qualifiers
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                                                                                                                       strain="W22"
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smulate meiotic recombination or homology-dependent repair at the
bz locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLN 26-PEB-2003
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Submitted (04-05C-2002) Waksman Institute, Rutgers University, Hoes
Lane, Piscateway, NJ 08855, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bikaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spamatophyta, Hagnoliophyta, Lilopsida, Poales, Poaceae; PACCAD Slade, Panicoideae, Andropsgoneae, Zea
             Direct Submission
Direct Submission
Submitted (0.1 9892, USA
Piscataway, NG 0892, USA
Location/Oualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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De novo origin of a tandem duplication in maize by improper resolution of a recombination intermediate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AY191010 8867 bp DNA linear PLN 26-
Zea mays BZ (Dp26)-ml bz locus tandem duplication sequence.
AY191016
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Pred. No. 0.026;
0; Mismatches 22; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="bz"
/note="duplicated integration site sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="duplicated integration site sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="Ac inserted into the Bz-McC allele"
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3 (bases 1 to 8867)
Zheng,Z., Martinez-Ferez,I.M. and Dooner,H.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'transposon="Activator (Ac)"
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Dooner, H.K. and Martinez-Ferez, I.M.
                                                                                                                                                                /organism="Zea mays"
/mol_type="genomic DNA"
/db xref="taxon:4577"
/chromoscme="9"
/map="95"
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                                                                                                                                                                                                                                                                                                                                                       /organism="Zea mays"
/mol_type="genomic DNA"
/db_xref="taxon:4577"
/chromosome="9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             allele="bz-m2(Ac)"
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1 Similarity 71.1%;
54; Conservative (
Fu, H. and Dooner, H.K.
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Best Local Similarity
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MEDLINE
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AY201779 407 bp DNA linear SYN 27-MAY-2003 Arabidopsis thaliana sequence flanking D83 end of D8-Trap insertion
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Spermatophyta, Magnotiophyta, udulocyledoms; core eudicots;
Gardis, Purceida, II; Brassicales; Brassicacese, Arabicopia.
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2. (Dasses 1 to 407)

May, B. p. Simcraweki, J., Arroyo, J.-M., Vaughn, M.W., Shen, R.,

May, B. p. Simcraweki, J., Arroyo, J.-M., Vaughn, M.W., Shen, R.,

Direct Shandsson, S. S.

Submitted (17-25C-2002) Cold Spring Harbor, My 11724, USA

Road, Cold Spring Harbor, My 11724, USA

http://genetrap.cohi.org/
                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 AGGGATGAAAACGGTCGGTAAACGGTCAGTAAAATACTACGGGATTTTTCCCATCCTACTT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 [bases 1 Co 407]
MMAy B. P. Simcrowski, J. Arroyo, J.-W., Vaughn, M.W., Shen, R.,
Arabiopsis, quanto sequences flanking be enhancer and gene traps
in transgenic lines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 AGGGATGAAAACGGTCGGTAACGGTCGGTAAATACCTCTACCGTTTTCATTTTCATATT 47
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
organism="Populus tremula x Populus tremuloides"
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                                                                                                                                                                                                                                                                                                                                                                            ry Match 14.9%; Score 40.4; DB 12; Length 197; ft Local Similarity 71.6%; Pred. No. 0.029; ches 53; Conservative 0; Mismatches 21; Indels 0;
                                                                                                                                                                           /note="transgenic line Esch5:358-Ac-rolC#3"
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|db_xref="taxon:3702"
|clone="GT5331.Ds3.04.24.00.b.407"
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/mol_type="genomic DNA"
/db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                             1.7.107
/transposon="Ac element"
                                                                                                                                                                                                   1. .107
/organism="Zea mays"
/mol_type="genomic DNA"
/db_xref="taxon:4577"
                        /mol type="genomic DNA"
                                                                                         /db xref="taxon:47664"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'ecotype="Landsberg"
                                                                                                          /sex="female"
/tissue_type="leaf"
/transgenic
                                                                 isolate="SK414"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana
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/transposon="transposon Ds"

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AF519991 The bp DNA linear SYN 14-JUL-2002 Populus tremula x Populus termuloides transpenito line Resensia Sea-Ac-rolcH3 isolate SK411 with Zea mays Ac element, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kumar, S. and Fladung, M. Somatic mobility of the maize element Ac and its usability for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 AGGGATGAAAACGGTCGGTAACGGTCGGTAAAATACTACGGGATTTTTCCCATCCTACTT 124
                                                                                                                                                                                                                                                                                                                                                                               Populue tremula x Populus tremmloides
Populus tremula x Populus tremuloides
Bostyces / Wirdiplatnes; Streprophyte; Entryophyte; Tracheophytes,
Spermetophyte; Marbollophyte; audioorphidons; core eudicots.
Spermetophyte; Marbollophyte; audioorphidons; core eudicots;
rocide; euroside; i; Authorbidhales; Salicacees; Populus.
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Pandir Mol. 1801. (2002) In press
2. Unbases 1 to 716)
Direct Submission
Submitted (Gr.UM: 2002) Bundesforschungsanstalt fuer Forst- und
Holywittechaft, Institut fuer Postgoatetk und
Postspilansmatuschitung, Saket Landsirsses 2, Grosshamsdorf 22927,
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                                                                                  66
                                                                                                                      Gaps
                                          Gaps
                                                                           /organism="Populus tremula x Populus tremuloides"
|/mol_type="genomic DNA"
|cultivar="Esch5"
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/note="transgenic line Esch5:35S-Ac-rolC#3"
                                          11; Indels
ch 14.9%; Score 40.4; DB 12;
1. Similarity 81.0%; Pred. No. 0.03;
47; Conservative 0; Mismatches 11;
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/mol_type="genomic_DNA"
/db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /isolate="SK411"
/db_xref="taxon:47664"
/sex="female"
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                                                                                                                                                                                                                                                                                                                                           AF519991.1 GI:21745065
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Best Local Similarity
Matches 47; Conserval
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALI GNMENTS

			sequence.	
			element	
			Ds	
			spl	
.7. 1 .066 AAA94066 standard; DNA; 271 BP.		30-JAN-2001 (first entry)	Arabidopsis thaliana sporocyteless spl Ds element sequence.	
AAA94066 ID AAA94066 sta	AAA94066;	30-JAN-2001	Arabidopsis	
REST AAAS ID	183	15	18	×

Sporocyteless; spl; meiocyte formation; plant sterility; seedless fruit; pollenless flower; Ds element; ds.

Sporocyteless nucleic acids and polypeptides, useful for controlling approcyte or matoryte formation in Jamies for producing transgenics that bear seedless fruits and/or pollaniess flowers.

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The present sequence is the coding sequence for the Arabinopsia thillaran approxycless (SPU) protein. This protein is involved in the formation of microsporovycles in family plants and meagesporovycles in female plants. The mitarity of grant was isolated from a collection of transpoante due to its male and female sterile phenotype. The mitarity is caused by the insertion of the Ds element between bases 411 and 412 of the grant insertion of the Ds element between bases 411 and 412 of the grant phenotype in plants caused by the insertion of this element means that it will be product ranspants of plants which contain the Ds element or antisence, may average the plants in the production of the plants and plants of the plants with the production of the section of the plants of the production of the plants with the production of seedless
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191 TCGGGTCAGGTTATGATCGACCCGGTTATTTCTCCATGGGGTTTTGTTGAGACCTCCTCC 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sporocyteless nucleic acida and polypeptides, useful for controlling approcyte or meiocyte formation in plante for producing transgenies that bear seedless fruits and/or pollenless flowers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 GGGCTACAAGGCTTCCCAAGCTCA-TCGGGAGCAACAGGATCTATTGTGGTGGAGTCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          410 GTGCTACAAGGCTTCCCAAGCTCACTCGGGAGCAACAGGATCTATTGTGGTGGAGTCGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3; Length 1302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fruits, pollenless flowers and plants with a larger biomass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1302 BP; 402 A; 273 C; 275 G; 352 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; L. 1.6e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.0%; Score 127.4;
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          Xu J;
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1. .2690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA94067 standard; DNA; 4071 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    product= "SPL"
      Yang W, Sundaresan V,
                                                                                                                                                                                                         Claim 2; Fig 2; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 98.6%;
Matches 139; Conservative
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                                             WPI; 2000-594578/56.
                                                                         P-PSDB; AAB26111
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                                                                                                                                              due to item male and female sterile phenotype. The mutation is caused by the insertion of the for themse themse have at land 41.00 the gene, publication of the sterile phenotype. The mutation of the sterile phenotype in plants caused by the insertion of this element means that it can be used to produce transpering plants which contain the be alment of an time and tenses esquences to the gane, enabling the production of seedless fruits, pollarless flowers and plants with a larger biomass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 ACTITICATCCGGGGCTACAAGGCTTCCCAAGCTCATCGGGAGGAACAAGGATCTATTGTGG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence comparises part of the coding sequence for the Arabidopsis thalians sporovreless (SPL) protein containing the De element. This protein is involved in the formation of sicrosporocyces in male plants and megasporovyces in feals to plants. The matern gene (containing the element) was isolated from a collection of transposants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sporocyteless, spl; melocyte formation, plant sterility, seedless fruit, pollenless flower, Ds element, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GTAGCATCGATCTCTAACAACGCTACCCGTTTACCCGGTACCGGGTAGCCCGGGTGTTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTAGCATCGATCTCTAACAACGCTACCCGTTTACCCGGTACCCGGGTGTTGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 271; DB 3; Length 271; 100.0%; Pred. No. 4e-88;
                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana sporocyteless spl coding sequence.
                                                                                                                                                                                                                                                                                                                                       Sequence 271 BP; 57 A; 71 C; 69 G; 74 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /transl_except= (pos:146. .148,aa:Lrg)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 GACCTCCTCCACTACTCATGAGCTCTCTTCA 271
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80. .1024
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/product= "SPL"
Çlaim 4; Pig 1A; 65pp; English.
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190 469

Gaps

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us-09-701-023-2.51304.rng

Xu J; Yang W, Sundaresan V, Ye D,

WPI; 2000-594578/56.

Sporocyteless nucleic acids and polypeptides, useful for controlling prococyte or milocyte formation in plantes for producing transgenics that bear seedless fruits and/or pollentess flowers.

Claim 45; Fig 5; 65pp; English

The present sequence comprises the promoter and coding sequence for the Arabidopsis thaltane sporcyaless (95%) protein. This profess is a megasprocycyles (195%) protein. This profess is a megasprocycyles (195%) protein a mean is protein a from a form of the mean is protein and the mean is a caused by the insertion of the abid mean efficiency of the series of the mean and the mean is a caused by the insertion of the series the produce transporting plants of this element means that it can be used to produce transporting plants with contain the De element or antisense sequences to the special canability the production of seedless fruits, polishes flowers and plants with a

Sequence 4071 BP; 1306 A; 742 C; 692 G; 1331 T; 0 U; 0 Other;

1; Gaps 1; 132 GOGCTACAAGGCTTCCCAAGCTCA-TCGGGAGCAACAGGATCTATTGTGGTGGAGTCGGG 190 Score 127.4; DB 3; Length 4071; Pred. No. 2.7e-35; 0; Mismatches 1; Indels 1; 47.0%; 98.6%; try Match st Local Similarity 98.65 ches 139; Conservative

191 TOGGGTCAGGTTATGATCGACCCGGTTATTTCTCCATGGGGTTTTGTTGAGACCTCCTCC 250

JA 3 3080 regestracertercareedecederrarrerecaredeserrrareadacerecede 3139

ABX93541 standard; DNA; 4810 BP

06-JUN-2003 (first entry)

DNA encoding the maize transposable element activator (Ac9).

Maize; da, transposable element activator; transcripton modification; pere repression; minimonalistication; pere repression; minimonalistication; pere repression; minimonalistication; descriptors; dispetes; dispetes; dispetes; dispetes; dispetes; dispetes; dispetes; dispetes; dispeted; dispeted; dispeted; dispeted; minitals dispetes; minimonalistication; delication; delicatio

Zea mays.

26-DEC-2002

The invention relates to a method of modifying (increasing, decreasing or altering) transcription within an organism or represent transcription of car least one targeted gone within a cell comprising introducing contrasting decreasing effector molecule into the organism or transposase encoding effector molecule into the organism or transposase encoding of effector molecule into the method is underlying a contrasting decreasing of activities of the method is underlying a contrasting decreasing of activities of the method is underlying an expension of the method is underlying the functions of unknown function of the method is useful for represent or an expression of the method is useful for represent or remark of the method is useful for represent or represent or represent or remark of the remark of th Modifying transcription within an organism or repressing transcription of targeted gene within a call, by introducing transposase-encoding effector molecule into organism or introducing transposase element into cell. Disclosure; Page 30-33; 46pp; English. 01-MAY-2002; 2002US-00138221 01-MAY-2001; 2001US-0287882P WPI; 2003-329235/31 (MACR/) MACRAE A P.

0; Gaps Sequence 4810 BP; 1390 A; 1063 C; 1063 G; 1294 T; 0 U; 0 Other; v Match 14.5%; Score 39.4; DB 7; Length 4810; Local Similarity 75.4%; Pred. No. 0,0033; Conservative 0; Mismatches 16; Indels 0; Query Match

AAI65447 standard; DNA; 4565 BP. AA165447;

The LATE

Nucleotide sequence of a maize activator element (AC).

10-DEC-2001 (first entry)

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The present expected regregates a reals Activator element (A), which is a transponshie element. 5' and 3' fragments of the present sequence were combined by Cloning to produce a synthetic De clement, which was used to produce the construct of the invention. The specification describes a mucleic acid construct of the invention. The specification describes a specific promoter operably linked to a maioride gene, both of which are linked to a sense of interappeans and the encoding mucleic acid, exid, The construct controls the unwanted speed of the construct controls the unwanted speed of
Activator element; Ac, transposable element; Ds element; transposon; gamete-specific promoter; suicide gene; gametophytic suicide trait; GST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hereologous traits in plants. It also provides genetic systems which can be used for the alimination of a quaecophytic audicide trust (GST) and for the selection of unlinked transpositions. The construct is applicable for any commercially grown plant, including fruit, seed, oil, protein or hay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               that selects against male or female gametes containing the suicide gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetic construct for the control of transgenes in transgenic plants comprises a sex specific promoter operatively linked to a suicide ger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      production, animal grazing, golf courses, lawns, erosion control, landscaping, green manure, producing food additives, pulp and wood production and smoking products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 73-74; 81pp; English.
                                                                                                                                                                                                                           28-FEB-2001; 2001WO-US006249.
                                                                                                                                                                                                                                                                    8-FEB-2000; 2000US-0185524P.
                                                                                                                                                                                                                                                                                                                                                             Moreno MA;
                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-602568/68.
                                                                                                                                                                                                                                                                                                                (UYYA ) UNIV YALE.
                                                                                                                                  WO200164926-A2.
                                                                                                                                                                                                                                                                                                                                                          Dellaporta SL,
                                                                                                                                                                              07-SEP-2001
                                                                                         Zea mays.
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Sequence 4565 BP; 1344 A; 994 C; 978 G; 1249 T; 0 U; 0 Other;

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65 AGGGATGAAAACGGTCGGTAACGGTCGGTAAATACTACGGGATTTTTCCCATCCTACTT 124
                                                                            AGGGATGAAAACGGTAACGGTAACGGTAGAAAATACCTCTACCGTTTTCATTTTCATATT 61
                             Gaps
                               ő
14.4%; Score 39; DB 4; Length 4565;
                             15; Indels
               0.0045;
                             0; Mismatches
             Pred. No.
           76.2%;
                          48; Conservative
           Local Similarity
                                                                                                             125 TCA 127
                                                                                                                                             64
                                                                                                                                           62
Query Match
                          Matches
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ds; transcription modification; gene repression; antibiotic resistance; human gamete; transplant: shoot, heart disease; phenylkochouria; Alzhokhew's disease; aging; emphysema; cancer; osteoporosis; diabetes; alsep apnea; sickle cell anaemia; stroke; multiple solerosis; misculae répstrophy; burstitis; diverticular disease; glaucoma; blindness; cataract; attention deficit disorder; dyslexia; hypertension;
                                                                                                                                                       Transposable element associated nucleic acid.
                  ABX93542 standard; DNA; 4565 BP.
                                                                                                            06-JUN-2003 (first entry)
                                                                ABX93542;
ABX93542/c
                                                                                      X5X5X5X5X5X
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RESULT 6

meart attack; alleigy; baldness; metabolic disorder; blood clotting; heemoplis; transassemis; sucromains disorder; blood clotting; pregrancy sesociated disease; infertility; obesity; gastroenteritis; immune system disorder; blood cell strice analysis reconsistion disease; monthal sucriou; policy; spinal cord disorder; pitulicary gland disorder; monthal sucress; spinal cord disorder; pitulicary gland disorder; manna, cartilomopathy; spinal cord disorder; pitulicary gland disease; manna; cartilingopathy; spinal cord disorder; pitulicary gland disease; manna; cartilingopathy; spinal cord disorder; pitulicary gland disease; schizophrenia; depression; bulimia nervosa; migraine; anorexia nervosa;

Unidentified.

US2002199216-A1.

26-DEC-2002.

01-MAY-2002; 2002US-00138221.

01-MAY-2001; 2001US-0287882P.

MACR/) MACRAE A F.

Macrae AF;

WPI; 2003-329235/31

It in act

Wodifying transcription within an organism or repressing transcription of targeted gene within a cell, by introducing transposace-encoding effector ancleoule into organism or introducing transposace element into cell.

Disclosure; Page 34-37; 46pp; English.

can

The invention relates to a method of modifying (increasing, decreasing or alleging and an examinant an examinance repressing transcription of cat learn on exerging does with an examinance repressing transcription of transposase element into the call. The method is useful for modifying a circumposase element into the call. The method is useful for pressing decreasing or alecting transcription within an organism of the method is useful for repressing a repressing transcription of the method is useful for pressing a respect gones within an organism. The method is useful for repressing transcription of expense of the method is useful for repressing transcription of the method is also useful for method is also useful method is also useful for method is method is also useful for method is also useful for method is also useful for method is method is also useful for method is also useful for method is also useful for method is present sequence is shown in Parkinson's disease, osteoarthritis, cystic fibrosis, arterial disease and cardiomyopathy. The present sequence represents the transposable element associated nucleic acid. Note: the present sequence is shown antigen recognition disease, nondisjunction, epilepsy, obesity, gastroenteritis, spinal cord disorders, pituitary gland disorders, obesity, 2 the appendix of the specification but no reference is made elsewhere in the specification

Sequence 4565 BP; 1249 A; 978 C; 994 G; 1344 T; 0 U; 0 Other;

Gaps ő DB 7; Length 4565; 0.0045; ~hes 15; Indels Pred. No. 0.00 0; Mismatches Score 39; 14.4%; 48; Conservative Local Similarity Query Match

Matches

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125 TCA 127

us-09-/01-023-2.51304.rng

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The invention relates to isolated polymocleotide (1) and polypeptide (11) sequence. (11) is useful as hypothastain probes, polymerase on habitance and un recombinant reduction (120) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (11). The polymocleotides are also used and in recombinant production of (11). The polymocleotides are also used genes. (1) is useful in gene therspy techniques to restore monal activity of ill or to treat disease states involving (11). (11) is useful in generalizing antiquence against the control of the properties of the properties
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ery Match 12.0%; Score 32.4; DB 5; Length 495; St Local Similarity 52.2%; Pred No. 0.43; Expension 72; Conservative 0; Mismatches 66; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 495 BP; 97 A; 141 C; 116 G; 141 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding novel human diagnostic protein #14709.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 14709; 103pp; English.
                                                                                                                                                                                                                                1905/c
AAS78905 standard; cDNA; 495 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-FEB-2002 (first entry)
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P-PSDB; ABG14718.
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4504 TAA 4502
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187 COGGICGGGICAGGITATGAICGACCCGGITATTICICCAIGGGGTTTTGTTGAGACCIC

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127 ATCCCGGGCTACAAGGCTTCCCAAGCTCATCGGGAGCAACAGGATCTATTGTGGTGGAGT 186

11.7%; Score 31.6; DB 4; Length 2692; 52.2%; Pred. No. 1.8; tive 0; Mismatches 64; Indels 0

Query Match 11.7 Best Local Similarity 52.2 Matches 70; Conservative

Sequence 2692 BP; 654 A; 794 C; 686 G; 558 T; 0 U; 0 Other;

Gaps

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The invention relates to an isolated mulcic acid detection resignation resignation of the detection of the control of the cont

New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell

Myers EW;

PWD,

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Venter JC, Adams M, WPI; 2001-656860/75. (PEKE) PE CORP NY.

23-MAR-2000; 2000US-0191637P. 11-JUL-2000; 2000US-00614150. 23-MAR-2001; 2001WO-US009231

Claim 1, SEQ ID NO 9214; 21pp + Sequence Listing; English

Drosophila, developmental biology; cell signalling; insecticide;

pharmaceutical; gene; ds. Drosophila melanogaster.

WO200171042-A2

27-SEP-2001

Drosophila melanogaster genomic polynucleotide SEQ ID NO 9214.

(first entry)

26-MAR-2002

ABL19247;

ABL19247 standard; DNA; 2692 BP.

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The invention relates to an isolated nucleic acid detection reagent cupple of detection relations of the companies of the companies of the invention is useful in developmental biology and in elucidating cell signalling and selected in the reactions in higher elactories of the development of insections in higher elactories of the development of insections in the relations of the development of a stations genome. On the parameter lating is the invention of selections genome (build of a selection of the parameter (build of a selection of the parameter (build of a selection of the parameter (build of a selection of the principal of parameter (build of a selection of the principal of a selection of the principal of a selection of the parameter of the principal of the companies of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127 ATCCCGGGCTACAAGGCTTCCCAAGCTCATCGGGAGCAACAGGATCTATTGTGGTGGAGT
                                                                                                                                                                                                                                               Drosophila, developmental biology, cell signalling, insecticide,
                                                                                                                                                                                        Drosophila melanogaster genomic polynucleotide SEQ ID NO 11668.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 11668; 21pp + Sequence Listing; English.
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         ABL20065 standard; DNA; 3037 BP.
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ID ABL28824 standard; DNA; 3308 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                               pharmaceutical; gene; ds
                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster.
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nes 70; Conserv
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                                                                                                                            26-MAR-2002
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                                                                     ABL20065:
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention: relates to an isolated mucleic and detection reagent capable to of detecting 1000 or more genee from Drosophila. The invention is useful in developmental blokogy and in elucidating cell signallian and coll-cell interactions in higher makeryores for the development of inspectic des. therapeutics and pharmaceutical trugs. The invention disclasses genomic makes expences (ARAD184 or NAM sequences (ARAD184 or NAM sequences (ARAD184 or NAM sequence) and the encoded proceding (ARBS773). Page sequence and at for this patient of inos (one past of the patients) proceding part of the patients of page of the page 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187 CGGGTCGGGTCAGGTTATGATCGACCCGGTTATTTCTCCCATGGGGTTTTGTTGAGGACCTC 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster genomic polynucleotide SEQ ID NO 37918.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 37918; 21pp + Sequence Listing; English.
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Pred. No. 1.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Myers EW;
                                                                                                                                                                                                          ABL28815 standard: DNA: 2971 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                              2560 GTCCCCATCTCATG 2573
247 CICCACTACTCATG 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 11.7%;
1 Similarity 52.2%;
70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2839 GICCCCATCTCATG 2852
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pharmaceutical; gene; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PEKE ) PE CORP NY.
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                                                                                                                                                                                                                                                                      ABL28815;
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ABL20065
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Gaps

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Drosophila; developmental biology; cell signalling; insecticide;
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pharmaceutical; gene; ds.
                                               Drosophila melanogaster.
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WO200171042-A2

23-MAR-2001; 2001WO-US009231 27-SEP-2001

23-MAR-2000; 2000US-0191637P. 11-JUL-2000; 2000US-00614150

(PEKE) PE CORP NY.

Myers EW; Li PWD, Adams M, Venter JC,

WPI; 2001-656860/75

New isolated nucleic acid detection reagent for detecting 1000 or more gene from Drosophila and for elucidating cell signaling and cell-cell interactions.

Claim 1; SEQ ID NO 37945; 21pp + Sequence Listing; English.

The invention realese to an isolated nucleic and detection reagent oppole of detecting 1000 or more genes from Droscophila. The invention in useful in developmental blology and in elucidating cell signalling and coll-cell interactions in higher cakeryotes for the development of insecticides, therspearled and pharmaceutical drugs. The invention of discloses genemic DNA sequences (ABLIG179 and the encoded proceding Approximation ABB7737). ABB72012. The sequence data for this patent did not foo mat direction printed specification, but was obstained in selectronic format directly from WIND or fitp. Wilpoli/published_pot_sequences.

Sequence 3308 BP; 898 A; 727 C; 732 G; 951 T; 0 U; 0 Other;

Gaps ; 11.7%; Score 31.6; DB 4; Length 3308; 52.2%; Pred. No. 2; tive 0; Mismatches 64; Indels 0; Local Similarity 52.2 ry Match

2827 cceccesascrescrarcasccacados as a subsecentra de constructor de consecue de constructor de 187 COGGICGGGICAGGITAIGAICGACCCGGITAITICICCAIGGGGITITGITGAGACCIC 246

JT 12 3064/c

ABL20064 standard; DNA; 10400 BP.

ABL20064;

(first entry) 26-MAR-2002 Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical; gene; ds

Drosophila melanogaster genomic polynucleotide SEQ ID NO 11665.

Drosophila melanogaster.

WO230171042-A2

27-SEP-2001

23-MAR-2001; 2001WO-US009231

23-MAR-2000; 2000US-0191637P. (PEKE) PE CORP NY EW; Myers Li PWD, Adams M,

New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell WPI; 2001-656860/75.

Claim 1; SEQ ID NO 11665; Zlpp + Sequence Listing; English.

The invention realese to an isolated nucleic date detection reagent opposed of detection of nuclear and an isolated nucleic and detecting flow or wore genes from Drosephila. The invention useful in developmenta librology and in a teludishing cell segmalling and cell-cell. Interesticions in higher enkaryotes for the development of insecticides, herspectical and pharmaceutical drugs. The invention distribution of the companion of the process genomic DNA sequences (ARLIGITS-ARLIGIS), expressed DNA ARRIVOTS). The sequence data for this patent did not form part of the printed specification, but was obtained in settomic formed directly from MINTO ar FUR PARTY OF the PRINT OF FUR PARTY OF the published population in settomic formed directly from MINTO ar FUR PARTY OF The PARTY OF T

Sequence 10400 BP; 2886 A; 2139 C; 2340 G; 3035 T; 0 U; 0 Other;

Gaps ö Ouery Match Best Local Smilarity 92.2%; Pred. No. 3.2; Natholos Matches 70; Conservative 0; Mismatches 64; Indels 0;

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187 CGGGTCGGGTCAGGTTATGATCGACCCGGTTATTTCTCCCATGGGGTTTTGTTGAGACCTC 246 g ò

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ABL28814/c

ABL28814 Standard; DNA; 10418 BP.

ABL28814,

(first entry) 26-MAR-2002

Drosophila; developmental biology; cell signalling; insecticide; Drosophila melanogaster genomic polynucleotide SEQ ID NO 37915

pharmaceutical; gene; ds Drosophila melanogaster.

WO200171042-A2.

27-SEP-2001

23-MAR-2001; 2001WO-US009231.

23-MAR-2000; 2000US-0191637P. 11-JUL-2000; 2000US-00614150.

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1253 ATCAACGACATCATCGTGCCACGCCCACAGCGCCACACAGCAGCGCGCCCCAGCTGATC 1194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1193 CCGCCCGGAGCTGGCTATCAGCCACAGGCGATTTCGATGTCTTCTTCTGAGCGGTGCTC 1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 ATCCCGGGCTACAAGGCTTCCCAAGCTCATCGGGAGCAACAGGATCTATTGTGGTGGAGT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chicken acetylglucosamine transferase VI (Gnt VI) protein encoding cDNA.
                                                                                                                                  The invention relates to an isolated mucleic acid detection reagent capable of detecting 1000 or more genes from Dorosphila. The invention useful in developmental biology and in alunidating cell cell interactions in Migher enkayores for the development of insertices, therapeutics and pharmaceutical drugs. The Invention discloses genomic DNs appentes (Mighlis for-ABBASSII), expressed DNN sequences (Mighlis for-ABBASSII), expressed DNN ABBASTOT2. The sequence and act for this pacent did not form part of the prince day specification, but was obtained in electronic format directly
New isolated nucleic acid detection reagent for detecting 1000 or more genee from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187 CGGGTCGGGTCAGGTTATGATCGACCGGTTATTTCTCCATGGGGTTTTGTTGAGACCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "acetylglucosamine transferase VI protein"
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10451 BP; 2904 A; 2145 C; 2346 G; 3056 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                              11.7%; Score 31.6; DB 4; Length 10451; NB 4; S2.2%; Pred. No. 3.3; Onservative 0; Wismatches 64; Indels 0;
                                                                                          Claim 1; SEQ ID NO 9211; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                       from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 5; Page 11-13; 22pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'product= "Gnt VI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABQ79896 standard; cDNA; 1395 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 70; Conserv
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                                                                                                                                                                                                                                                                                              The invention relates to an isolated mucleic acid detection reagent capable of detecting 1000 on more gases from prosphila. The invention is userful in developmental biology and in elucidating cell signalling and call-cell interactions in higher enhancement of inserticides, therepeutice and pharmaceutical drugs. The invention of inserticides, therepeutice and pharmaceutical drugs. The invention of SIGNORS generic MAILSTS (76.4813011). Appressed DNA sequences (MAILSTS) and the encoded proceins (MAILST) part of the prince specification, but was obtained in electronic formed directly princed specification, but was obtained in electronic formed directly
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                                                                                                                                                           New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.7%; Score 31.6; DB 4; Length 10418; 52.2%; Pred, No. 3.3; cive 0; Mismatches 64; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster genomic polynucleotide SEQ ID NO 9211.
                                                                                                                                                                                                                                                         Claim 1, SEQ ID NO 37915; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                    Myers EW;
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                                                                    Li PWD,
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                                                                    Adams M,
                                                                                                                PI; 2001-656860/75.
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                     (PEKE ) PE CORP NY.
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                                                                                                                                                                                                          Interactions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila;
                                                                    Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      187
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The invention relates to a protein having accept/glucosanian transferase VI (GRt VI) activity and polymuclecides encoding the GRt VI protein. The protein can be expressed by standard recombinant methodoly. GRt VI is useful if coractlysing the transfer of GloWat to the 4th site of Wan alpha A. i. 6 arm of the oose structure of Najuran. The present sequence Man alpha represents the chicken GRt VI protein colding sequence Sequence 1395 BP; 280 A; 444 C; 366 G; 305 T; 0 U; 0 Other;

1143 CIGCACCCGGACGCGGGGGACACGGCTGGTGGAGAAATGGAGAAAATGCTGCC 1084 0; Gaps ry Match 11.44; Score 30.6; DB 6; Length 1195; it Local Similarity 48.84; Pred. No. 2.6; S. Corservative 0; Mismatches 87; Indels 0;

95 AAATACTACGGGATTTTTCCCATCCTACTTTCATCCCGGGCTACAAGCTTCCCAAGCTC 154

;h completed: May 16, 2004, 13:08:25 :ime : 403 secs

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TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Two Embarcade
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
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9999999999999999
                                                                                                                                                                                                                                                                                                                                                                                                         US-08-475-891A-3/c
Sequence 3, Appl. Sequence 11017, A Sequence 11017, A Sequence 1105, A Sequence 2, Appl. Sequence 2, Appl. Sequence 1127, Appl. Sequence 2, Appl. Sequence 2
                                                                                                                   May 16, 2004, 12:43:45; Search time 75 Seconds (without alignments) 2005.223 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Listing first 45 summaries
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GENERAL INCOMMING.

APPLICANT: VAN. Chumha et al.

TITLE OF INVENTION: ACID MULECULES ENCODING HOWAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: ACID MULECULES ENCODING HOWAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

CHARLES REFERENCE: COLOD1098

CHARLES TELING DATE: 2001-03-09

FOR THE OF THE OF THE COLOTION NONDERS: US 009/801,861
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10.1%; Score 27.4; DB 4; Length I

Bett Local Similarity 51.2%; Pred. No. 3;

Matches 64; Conservative 0; Mismatches 61; Indels
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         ; TYPE: DNA
; 'ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13017
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ORGANISM: Pseudomonas aeruginosa
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US-09-25-991A-12771/C
US-09-25-991A-12771/C
Sequence 1271-Application US/09252991A
Parent No. 6551/95
CENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: UNUMER: US/09/25, 991A
CURRENT PAILOR DATE: 1099-02-18
PRIOR PRIOR DATE: 1399-02-18
PRIOR PLICATION NUMER: US 60/094, 788
PRIOR PLICATION NUMER: US 60/094, 788
PRIOR PLICATION NUMER: US 60/094, 180
PRIOR PLICATION NUMER: US 777
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Sequence 11017 197.

Sequence 11017 197.

Becaut No. 655179 Spalication US/09252991A

Percent No. 655179 Spalication US/09252991A

TITLE OF INVENTION: NUCLEIC ACID AND ANIMO ACID SEQUENCES PELATING TO PSEUDOMONAS

TITLE OF INVENTION: ASSULINGES FOR INGANGETICS AND THERAPPHICS

TITLE OF INVENTION: ASSULINGES FOR INGANGETICS AND THERAPPHICS

CURRENT APPLICATION NUMBER: US/09252.991A

PRIOR PILING DATE: 1999-02-18

PRIOR PAILCATING DATE: 1999-02-18

PRIOR PAINTED DATE: 199
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                                                                                                                                                            Score 29; DB 2; Length 5992;
Pred. No. 2;
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US-09-252-991A-13017
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                                              US-08-475-891A-3
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ORGANISM: Pseudomonas aeruginosa
                                                                    US-09-252-991A-12220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
LE REFERENCE: UMO1523
                                                                                                                                                                                                                                                                                                                                                                                                                                       13 TCTAACAACGCTACCCGTTTACCCGTACCGGTAGACCCGGGTGTTGTGCTACAGGGATGA
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Pred. No. 50;
0; Mismatches 36; Indels 0:
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                                                                                                                                                                                                                                                                                 Length 53332;
                                                                                                                                                                                                                                                                           Score 27.4; DB 4; Length 5
Pred. No. 27;
0; Mismatches 36; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IRRENT APPLICATION NUMBER: US/09/497,85SA
RERNT PELING APPLE: 2000-20-04
LIOR APPLICATION NUMBER: 60/10,592
LIOR PLILING DATE: 1999-02-18
LIOR APPLICATION NUMBER: 60/118,760
LIOR APPLICATION NUMBER: 60/118,760
FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17770 AAGCATGGGGTAAAGAACTGTTGAA 17746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 CTACGGGATTTTCCCATCCTACTT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tuence 12220, Application US/09252991A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 AAACGGTCGGTAACGGTCGGTAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3-497-855A-40/c
Tuence 40, Application US/09497855A
ent No. 6605432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MBER OF SEQ ID NOS; 54
PTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 10.1%;
1 Similarity 57.6%;
49; Conservative (
                                                                                                                                                                                                                                                                           th 10.1%; 1 Similarity 57.6%; 49; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YPE: DNA
RGANISM: Homo sapiens;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERAL INFORMATION:
PPLICANT: Huang, Tim
                                                                                                                                                                                                                                                                           iry Match
it Local Similarity
:ches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ary Match
at Local Similarity
ches 49; Conserv
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                                                                                                                TYPE: DNA
DRGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH: 161652
                                                                                53332
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PTWARE:
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GREEN W. WORKSTON CONTRIBUTION OF THE WATER 
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                                                                                                                                                                                                  215 TWCCMACCMACCMRRARECOMRSCHRSYTYMMCYYYYWMYYKGGRAYWWWRGGMWKRMYW 274
                                                                                                                                                                                                                                                                             635 ACCCIGCACCATCATCACAATCACGACGATCACGTGCGAACGCCCTTGACACTC 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 ACGGICGGINACGGICAGAAAJACJACGGGAJTITITCCCATCCTACTITCATCCCGGG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        275 MYKKKSMWKGSCMWKRAWWARKTTYYTWAWYYTTYYKRMÒCYYMRKTTYCHMMWYSRWWR 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 TAACAACGCTACCCGTTTACCCGTACCGGTAGACCCGGGTGTTGTGCTACAGGGATGAAA 74
Score 27.2; DB 4; Length 948;
Pred. No. 3.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.0%; Score 27; DB 4; Length 474 17.6%; Pred. No. 2.8;
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Best Local Similarity 17.6%; Pred No. 2.8; Indels
Matches 27; Conservative 63; Mismatches 63; Indels
                                                                                                 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: ESFS and Encoded Human Proteins. FILS REPERMOR. ENSINET. OSEP PRAZ. CURRENT APPLICATION NUMBER: US/05/621,976
CURRENT FILING DATE: 2000-07-21
WHORER OF SEX ID NOS: 19335
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 CTACAAGGCTTCCCAAGCTCATCGGGAGCAACA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              335 GSMWTARGAWWNCYWWYYWAARKKKKWWWAAA 367
                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2128, Application US/09134001C
Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18033, Application US/09621976
Patent No. 6639063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Dumas Minne Edwards, J.B.
APPLICANT: JOBET, S.
APPLICANT: Glordano, J.Y.
                                                                                                                                                                                                                                                                                                                                                                                                     200 GTTATGATCGACCCGGTTAT 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 16 7 CTHER INFORMATION: n=a, g, c or t US-09-621-976-18033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       575 Treerearesceecedar
       10.0%;
                                                                                                        47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-134-001C-2128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 474
              Query Match
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                                                                                                        Matches
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134 GCTACAAGGCTTCCCAAGCTCATCGGGAGCAACAGGATCTATTGTGGTGGAGTCGGGTCG 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1 Application US/0975426

GENERAL PROPERTION 6772527

GENERAL PROPERTION 1 ENGLATE HANA PROSPROISSTERASE

TITLE OF INVESTION 1 ENGLATE HANA PROSPROISSTERASE

TITLE OF INVESTION 1 PROFINGING, NUCLEIC ACID MOLECULES RECODING HUMAN

TITLE OF INVESTION 1 PROFINGING, NUCLEIC ACID MOLECULES FREEDOF

CHREEN PELICACION NUMBER: US/09/754,250

CURRENY PELICAC DATE: 2001-05

SOUPHARS: PELICAC SECTION 1003

SOUPHARS: PELICAC SECTION 1003
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1 Similarity 56.0%; Pred No. 58;
1. Conservative 0; Mismatches 40; Indele 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 GGTCAGGTTATGATCGACCCGGTTATTTCTCCATGGGGTTTTGTTGA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208 AGTCATATGCAGCTCAAGCCACGTTTTTCTCTAAAAGCTTGACTTGA 254
                                                                                     NAMS/KEY: primer bind
LOCATION: 1854..1873
OTHER HIFORMATION: upstream amplification primer, complement
PERTURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Omery Match 10.0%; Score 27; DB 4; Length 3001; Best Local Similarity 53.3%; Pred. No. 7.5; Matches 57; Conservative 0; Mismatches 50; Indels
                                                                                                                                                                                                                    NAME/KEY: primer_bind
LCCATION: 1391..1411
CLORE INFORMATION: downstream amplification primer
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108159 GTCTGCAAACAGCCCCATGGGGGAGGACTGG 108129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 GGGAGCAACAGGATCTATTGTGGTGGAGTCG 188
                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_binding

// LOCATION: 1489...1513

// OTHER INFORMATION: 99-25961-376 probe
    LOCATION: 1481..1500
OTHER INFORMATION: 99-25961-376.mis2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2813, Application US/09621976
Patent No. 6639063
GENERAL INPORMITION:
APPLICANT DUMBS WALLE Edwards, J.B.,
APPLICANT Obsert, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: (1) ... (111282)
; OTHER INPORMATION: n = A,T,C or G
US-09-754-250-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
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Matches 51; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 3
LENGTH: 111282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: GOMESTAND TO COMMARKAY, 11ya
APPLICANT: GOMESTAND TO COMMARKAY, 10ya
TITLE OF INTERFERENCE COMMARKA: 10ya
APPLICANTON NUMBER: US 60/126, 913
PRIOR APPLICANTON NUMBER: US 60/126, 915
PRIOR APPLICANTON NUMBER: US 60/126, 915
PRIOR APPLICANTON NUMBER: US 60/146, 453
PRIOR APPLICANTON NUMBER: US 60/146, 384
PRIOR PLINKO DATE: US 90/146, 384
                                                                                                                                                                                                                                                                                                                                                                                                   157 GTAGCAGCATTAACACCTAAAGCTGAAATTGAAGGTGAAATGGGAGATACTCATGTTGGT 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 CTACAGGGATGAAAACGGTCGGTAACGGTCGGTAAAATACTACGGGATTTTTCCCATCCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          517 TTACAAGCAAGATTAATGTCTCAAGCATTAAGAAGTTATCAGGGGCTATTTCTAAATCT 576
                                                                                                                                                                                                                                                                                                                                           1 GTAGGATCGATCTTAACAACGCTACCCGTTTACCCGTACCCGGTAGACCCGGGTGTTGTG 60
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                    Query March 10.0%; Score 27; DB 4; Length 1074; Bett Local Similarity 51.2%; Pred, No. 4.4; Marches 63; Conservative 0; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 1501
OTHER INFORMATION: 99-25961-376 : polymorphic base T or G
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LOCATION: 1502-1520
LOCATION: 1502-1520
                                                                                                                      , ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 127, Application US/095393330 Patent No. 4776208
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 2128
LENGTH: 1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 ACT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     577 AAT 579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-539-333D-127
                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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Giordano,

STRANDEDNESS:

us-09-701-023-2.51304.rn1

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TOPOLOGY: linear;
MOLECULE TYPE: DNA
US-08-829-525-37
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                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 AACGGTCGGTAAAATACTACGGGATTTTTCCCATCCTACTTTCATCCCGGGCTACAAGGC 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  342 WWMKKKARRWYYWWKSTYACASRYRKYTWGWWWYMWRBWKSTRWYCYMCWKCCMYRGRRC 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WHEAL INFORMATION:
APPLICON: Levineon, Douglas A.
APPLICON: Levineon, Douglas A.
TILLE OF INVESTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVESTION: TREATMENT AND DIAGNOSIS OF INVENTION: TREATMENT AND DIAGNOSIS OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               iry Match 9.9%; Score 26.8; DB 4; Length 832; tr Local Similarity 13.3%; Pred. No. 4.6; chee 13; Conservative 54; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144 TICCCAAGCICATCGGGAGCAACAGGATCTATIGIGGT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           282 AWYTWARGRWWSYAWGKWKSMRSAMSMCTRMYYKKGST 245
       LIE REFERENCE: GENERAL COMPAGE AUMAND Proteins.
LIE REFERENCE: GENERAL C54FR2.
RRENT APPLICATION INVERSE: US/09/621,976
RRENT PILING DATE: 2000-07-21
RRENT SERVENT 
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
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PELLING DIREC 01-682-1996
APPLING DIREC 01-682-1996
APPLING DIREC 01-682-1996
APPLING DIREC 07-001-1995/4627
APPLING DIREC 07-001-1995/4627
APPLING DIREC 03-601-1995
APPLING DIREC 03-601-1995
APPLING DIREC 03-601-1995
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FILING DATE: 28-MAR-1997
CLASSIFICATION: 536
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TELECOMMINICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nence 37, Application US/08829525
ent No. 6084083
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SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELERANE: 212-669-9990
TELEX: 6614 PERNIE
TELEX: 6614 PERNIE
SEQUENCE CHARACTERISTICS:
LENGTH: 993 Base pairs
TFFE: nucleac acad
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                              >RGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: New York
STATE: New York
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OCATION: 235..399
9-621-976-2813
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84 AACGGICGGIAAAAIACIACGGGIITITICCCAICCIACTIICAICCGGGGIACAAGGC 143
                                                                                                                                                                            380 AACTICAĞĞITAAAİTTİTCATCAİTCAİTATGCCTGGGAİTITGGALCCĞĞCAĞCAĞIAĞ 321
                                                                                                                                                                                                                                       144 TTCCCAAGCTCATCGGGAGCAACAGGATCTATTGTGGTGGAGTCGGGTCGGGTTA 203
                                                                                                                                                                                                                                                                                              320 ArcccacreterecradaGreacatrereridareaGreacacacacretererreceGaAA 261
                                                                                                                                                                                                                                                                                                                                                             204 TGATCGACCCGGTTATTTCTCCCATGGGGTTTTGTTGAGACCTCCTCCTCCTACTCATGAGC 263
                                                                                                                                                                                                                                                                                                                                                                                                      260 rcccarrradccagrarcradadrecaaraarrcacarccrrrcarcarccrade 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108-609-503-59A-37/C
Paragrance 37, Application US/O8609583A
Paragrance 37, Application US/O8609583A
Paragrance 37, Application US/O8609583A
APPLICANT: Levisson, Douglas A.
APPLICANT: Levisson, Douglas A.
TITLE OF UNEXTION: CORPOSITIONS AND MERIODS FOR THE
TITLE OF PROPERTIONS TO THE THE TABLE OF THE THE TABLE OF SUCCESS.
ch 9.94; Score 26.8; DB 3; Length 903;
1. Similarity 46.74; Pred. No. 4.8;
85; Conservative 0; Mismatches 97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 1005/E7111
ZIP: 1005/E7111
MEDING TYPE: Diskete
COMPUTER: 1BM Compacible
OFFRATING SYSTEM: DOS
SOFTWARE: FaceSEQ Version 2.0
GURBRY APPLICATION DATA
PLICATION NUMBER: 01-088
FILING DATE: 01-088-1996
CLASSIFICATION N
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PRIOR APPLICATION NOTA:

FILING DATA:

MARX-195

MATCHER DATA:

MARX-195

MARX-195
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ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 30,742
REPERENCE/DOCKET NUMBER: 78
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 903 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York
STATE: New York
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84 AACGGTCGGTAAAATACTACGGGATTTTTCCCATCCTACTTTCATCCGGGCTACAAGGC 143
                                                                                                                                                                                204 TGATCGACCCGGTTATTTCTCCATGGGGTTTTGTTGAGACCTCCTCCACCACCTACTCATGAGC 263
                                                                                                                                                                                                                                                                                                                260 TCCCCATTTAGCCAGTATCTGGATGTCCCATAATTCACATCCCTTTCATCAGTCCTGAGC 201
                                                                                                                                      380 AACTTCAGGTTAAATTTTTTCATCATTCATTATGCCTGGGATTTGGATCCGGCAGCAGGTAG 321
                                                                                                                                                                                                                             320 Arcccacrercrectasagreacantercreansereassagaearcreerrecessaa 261
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Levinean, Douglass A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF IMMONE DISORDERS
NUMBERS OF SEQUENCESS: 37
CORRESPONDENCE ADDRESS:
                                                   ö
Query Watch 9:9%; Score 26:8; DB 3; Length 903; Best Local Similarity 46:7%; Pred. No. 4.8; Machae B5; Conservative 0; Mismatches 97; Indels Matchae 85; Conservative 0; Mismatches 97; Indels
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46.7%; Pred. No. 4.8;
tive 0; Mismatches 97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/609,583
FILING DATE: 01-MAR-1996
APPLICATION NUMBER: US 08/487,748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 07-UN-1995
FILING DATE: 08-04396,633
FILING DATE: 03-WAR-1995
FILING DATE: 03-WAR-1995
NAME: COURZE, Laura A.
REGISTRATION NUMBER: 30,732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: FastESQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 7853-048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . Sequence 37, Application US/08937399
; Patent No. 6288218
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OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INPORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 903 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 46.7
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10036/2711
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New York
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US-08-937-399-37/c
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Gaps

97; Indels

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320 ATCCCACTGTCTGCTAGAGTCACATTCTCTATGGTCAGGGACACATCTCCTTTGCGGAAA 261
84 AACGGTCGGTAAAATACTACGGGATTTTTCCCATCCTACTTTCATCCGGGCTACAAGGC 143
                                                380 AACTICAGGITAAATTITICATCATTCATTATGCCTGGGATTITGGATCCGGCAGCAGTAG 321
                                                                                                          144 TICCCAAGCICATCGGGAGCAACAGGAICTATTGIGGIGGAGTCGGGICGGGTCAGGTTA 203
                                                                                                                                                                                                                         204 TGATCGACCCGGTTATTTCTCCATGGGGTTTTGTTGAGACCTCCTCCACTACTACATGAGC 263
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Job time : 79 secs
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

cleic - nucleic search, using sw model

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May 16, 2004, 13:01:51 ; Search time 393 Seconds (without alignments) 3129:291 Million cell updates/sec

1 gtagcatcgatctctaacaa......ctactcatgagctcttca 271 US-09-701-023-2 271 it ict score:

nce:

2947324 segs, 2269024515 residues IDENTITY NUC Gapop 10.0 , Gapext 1.0 ng table:

:peq:

number of hits satisfying chosen parameters: num DB seq length: 0 num DB seq length: 200000000

processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

ase:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by shalysis of the total score distribution.

SUMMARIES

Sequence 213704, Sequence 213704, Sequence 213704, Sequence 3402, Ap. Sequence 114961, Sequence 174961, Sequence 1666, App. Sequence 451, App. Sequence 451, App. Sequence 451, App. Sequence 451, App. Sequence 451, App. Sequence 451, App. Sequence 451, App. Sequence 451, App. Sequence 451, App. Sequence 451, App. Sequence 451, App. Sequence 18, App. Seq Sequence 3, Appli Sequence 8, Appli Sequence 213703, Sequence 6, Appli Description US-10-138-221-8 US-10-027-632-213703 US-10-027-632-213703 US-10-027-632-213703 US-10-027-632-213703 US-10-027-632-14961 US-10-027-632-14961 US-10-106-698-1663 US-10-006-285-506 US-10-087-192-451 US-09-919-497-18 US-10-138-221-6 US-09-794-384A-3 Query Match Length DB 11.4 3186778 11.4 3186778 11.1 1022 11 11.1 1759 11 10.9 256525 11 10.8 6746 9 12.3.3.3.4 112.3.3.3.4 112.3 Score

Sequence 303, App	Seguence	Sequence	Sequence		Seguence 1, Appli	Sequence 184451,	Sequence	Sequence 2603, Ap	Sequence 31702, A	Sequence 6, Appli	Seguence	Sequence	Seguence	Sequence 111889,	Seguence		Sequence	Sequence	Sequence	Sequence		Seguence 32797, A	Sequence 1319, Ap	ď,		Sequence 2240, Ap		Seguence 2	Sequence	Sequence 59064,
US-09-967-768A-303	US-10-085-117-10				US-10-402-072A-1					Þ		US-10-282-122A-37020							-			US-10-425-114-32797	US-09-764-869-1319	US-09-764-869-2240		US-10-091-504-2240	US-10-227-577-1319	US-10-227-577-2240	3 US-10-027-632-59064	.6 US-10-027-632-59064
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6746	36595	460	1434	4748	4748	502	502	2000	2689	19639	252	1314	1879	2778	2778	89625	597	684	684	684	684	1501	5519	5519	5519	5519	5519	5519	1601042	1601042
10.8	10.8	10.8	10,8	10.8	10.8	10.7	10.7	10.7	10.7	10.7	10.6	10.6	10.6	10.6	10.6	10.6	10.6	10.6	10.6	10.6	10.6	10.6	10.6	10.6	10.6	10.6	10.6	10.6	10.6	10.6
29.4	29.4	29.5	29.5	29.5	29.3	29	53	29	59	59	28.8	28.8	28.8	28.8	28.8	28.8	28.6	28.6	28.6	28.6	28.6	28.6	28.6	28.6	28.6	28.6	28.6	28.6	28.6	28.6
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ALIGNMENTS

Publication No. 082000193216A1
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APPLICANT: NAW 7. Meacae
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APPLICANT: NAW 7. Meac ö TYPE: DNA ORGANISM: Zea mays LENGTH: 4810 US-10-138-221-6 US-10-138-221-6

63 ACAGGGATGAAAACGGTCGGTAACCGTCGGTAAAATACTACGGGATTTTTCCCCATCCTAC 122 Gaps 0 Onery Match 14.5t, Score 39.4; DB 14; Length 4810; DB st Local Similarity 75.4t; Petel No. 0.018; Matches 49; Conservative 0; Mismatches 16; Indels 0;

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121 ATAGGGATGAAAACGGTCGGTAACGGTCGATAAATACCTCTACCGTTTTCATTTTCATA 180 123 TTTCA 127 TTTAN 185 US-09-794-384A-3 RESULT 2 윱 ઠ 셤

Sequence 3, Application US/09794384A Patent No. US20020144305A1

GENERAL INFORMATION:

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336 TCATCCTGACCTGSATGGTTGCCCCTGATCACTGGGAGCACGTGGGTTTGCTGTTATGTA 277
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TITLE OF INVESTION: Identification and Mapping of Single Nucleocide
TITLE OF INVESTION: Delymorphisms in the Human Genome
CURRENT PLINE NETRINGER: 10827, 1202-160-20
CURRENT PLINE DATE: 2000-02-04-20
PRIOR PAPLICATION NUMBER: US 60/18, 506
PRIOR PAPLICATION NUMBER: US 60/18, 606
PRIOR PAPLICATION NUMBER: US 60/19, 483
PRIOR PAPLICATION NUMBER: US 60/19, 483
PRIOR PAPLICATION NUMBER: US 60/19, 483
PRIOR APPLICATION NUMBER: US 60/19, 483
PRIOR APPLICATION NUMBER: US 60/16, 363
PRIOR APPLICATION NUMBER: US 60/16, 363
PRIOR APPLICATION NUMBER: US 60/16, 363
PRIOR APPLICATION NUMBER: US 60/16, 363
PRIOR APPLICATION NUMBER: US 60/16, 363
PRIOR APPLICATION NUMBER: US 60/146, 002
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52.6%; Pred. No. 0.12;
Live 1; Mismatches 62;
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SOFTWARE, FastSEQ for Windows Version 4.0
SEQ ID NO 213703
LENGTH: 533
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SOFTWARE: FBSESEQ for Windows Version 4.0
SEQ ID NO 213704
LENGTH: 533
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Publication No. US20020198371A1
GENERAL INFORMATION:
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Matches 70; Conservative
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US-10-027-632-213703
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4564 AGGGATGAAAACGGTCGGTAACGGTCGGTAAAATACCTCTACCGTTTTCATTTTCATATT 4505
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                      APPLICANT: Moreno, Maria A. APPLICANT: Yale University APPLICANT: Yale University Methods and Compositions to Reduce or Eliminate TITLE OF INVENTION: Transmission of a Transgene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cch 144%; Score 39; DB 14; Length 4565; Il Similarity 76.2%; Predc No. 0025; 48; Conservative 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
14.4%; Score 39; DB 9; Length 4565;
Best Local Similarity 76.2%; Pred. No. 0.0025.
Matches 48; Conservative 0; Mismatches 15; Indels
Matches 48; Conservative 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Transposable element Ac
                                                                                                     FILE REFERENCE: 44574-5079-US
CURRAY PAILLOYNON NUMBER: US/597794,384A
CURRAY FILING DATE: 2001-02-28
PRIOR PRILING DATE: 2000-02-28
NUMBER: 05 807 1055,524
NUMBER: 05 807 1055,524
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APPLICANT: Dellaporta, Stephen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                    SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 4565
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Best Local Similarity
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ORGANISM: Zea mays
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ORGANISM: Zea mays
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RGANISM: Human

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Gaps ö Length 533; 62; Indels Score 33.4; DB 13; Pred. No. 0.12; 1; Mismatches 62; rry Match 12.3%; it Local Similarity 52.6%; ches 70; Conservative

|-027-632-213703/c | puence 213703, Application US/10027632 | Application No. US20030204075A9 ERAL INFORMATION:

RGANISM: Human

-027-632-213703

12.3%; Score 33.4; DB 16; Length 533; 52.6%; Pred. No. 0.12; tive 1; Mismatches 62; Indels 0 iry Match
it Local Similarity 52.61
:ches 70; Conservative

125 TCATCCCGGGCTACAAGGCTTCCCAAGCTCATCGGGAGCAACAGGATCTATTGTGGTGGA 184

3.6 rcarccreaccresaregrieccccrearcacreecaceaceaceacegerriecrerarera 277 185 GTCGGGTCGGGTCAGGTTATGATCGACCCGGTTATTCTCCCATGGGGTTTTGTTGAGGACC 244

276 ACGGAGAAGGAGGAATGTATTGGCTCCCAGGTGATAAATGGGGGTGATTTCTTGGTACCT 217

JT 7, 3-027-632-213704/c

OTHER INFORMATION: Clone ID: 700264066 FLI

US-10-425-114-3402

TYPE: DNA ORGANISM: Zea mays

PEATURE:

SEQ ID NO 3402

Sequence 3422, Application US/10425114
Publication No. USZ0040034888A1
GENERAL REPORTATION: LOUGH CONTROLL REPORTATION: LOUGH CONTROLL REPORTATION: APPLICANT: APPLICANT: School Controller Scho 336 rearcerdacerdsanderneceergareacreedadeacerdeserrrecretrarera 277 185 GICGGGTCGGGTCAGGTTATGATCGACCCGGTTATTCTCCCATGGGGTTTTGTTGAGACC 244 276 ACGGAGAAGGAATGTATTGGCTCCCAGGTGATAGGGGGGTGATTTCTTGGTACCT 217 Sequence 213704, Application US/10027632
Publication Way, US20204078A9
Publication Way, US20204078A9
Publication Way, US20204078A9
Publication Way, US202040704
TITLE OF INVENTION Indentification and Mapping of Single Muclectide
TITLE OF INVENTION INDENTIFICATION USERS: US40707632
CURRENT PILLOR DATE: 2002-04-30
FRIOR APPLICATION WAYBER: US 60/128,676
FRIOR PAPLICATION WAYBER: US 60/128,676
FRIOR FILMO DATE: 2000-07-12
FRIOR FILMO DATE: 2000-03-29
FRIOR FILMO DATE: 2000-02-24
FRIOR APPLICATION WAYBER: US 60/165,368
FRIOR APPLICATION WAYBER: US 60/165,368
FRIOR APPLICATION WAYBER: US 60/165,368
FRIOR APPLICATION WAYBER: US 60/165,368
FRIOR APPLICATION WAYBER: US 60/166,368
FRIOR APPLICATION WAYBER: US 60/166,368
FRIOR APPLICATION WAYBER: US 60/166,368
FRIOR FILMO DATE: 1999-03-28
FRIOR FILMO DATE: 1999-03-28
FRIOR FILMO DATE: 1999-03-09
FRIOR FILMO DATE: 1995-03-09
FRIOR FILMO DATE: 1995-03-09
FRIOR FILMO DATE: 1995-03-09
FRIOR FILMO DATE: 1995-03-09
FRIOR FILMO WAYBER: US 60/146,002
FRIOR FILMO DATE: 1995-03-09
FRIOR FILMO WAYBER: US 60/146,002
FRIOR FILMO DATE: 1995-03-09
FRIOR FILMO DATE: 1995-03-09
FRIOR FILMO DATE: 1995-03-09
FRIOR FILMO DATE: 1995-03-09
FRIOR FILMO DATE: 2095-03-09
125 TCATCCCGGGCTACAAGGCTTCCCAAGCTCATCGGAACAGGATCTATTGTGGTGGA Gaps Length 533; Indels Score 33.4; DB 16; Pred. No. 0.12; 1; Mismatches 62; Best Local Similarity 52.6%; Matches 70; Conservative 245 TCCTCCACTACTC 257 216 cccrigcccaarrc 204 US-10-425-114-3402/c ORGANISM: Human SEQ ID NO 213704 LENGTH: 533 Query Match ઠ 윱

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APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypepti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 3186778;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47; Indels
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                                                                                        REIGN APPLICATION WHERE: 135 (0.1.99.7) FRICAL STREET TO THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTR
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Pred. No. 37;
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CURRENT APPLICATION NUMBER: US/10/106,698

CURRENT PELING DATE: 2002-03-27

PRIOR APPLICATION NUMBER: PCT/USO/265-34

PRIOR APPLICATION NUMBER: PCT/USO/265-34

PRIOR APPLICATION NUMBER: 1991-03-29

PRIOR APPLICATION NUMBER: US 60/157,137

PRIOR RAPLICATION NUMBER: US 60/157,137

PRIOR RAPLICATION NUMBER: US 60/153,280

NUMBER OF SD 1D NOS: 856-4
                                               PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-174961
                    2002-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vuery Match 11,4%;
Best Local Similarity 55.7%;
Matches 59; Conservative 0
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US-10-106-698-1963
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Matches 68; Conserva
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LENGTH: 1022
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                                                                                                                                                                                                                                                                        1785 AGGGATGAAAACGGTCGGAAACGGTCGGTAAACACCAAAACCATTACCGTTTTCATATTT 1726
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                                                                                              Gaps
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TILLE OF INVEXTION: Identification and Mapping of Single Mucleotide PITLE OF INVEXTION: Polymorphisms in the Human Genome PIT EXPERENCE: 10887,139
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             DB 13; Length 2360;
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                                                                                              18; Indels
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      Score 32.2; DB
Pred. No. 0.63;
0; Mismatches
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SOFTWARE: FastSEQ for Windows Vergion 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 174961, Application US/10027632
; Publication No. US20020198371A1
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Publication No. US20030204075A9
GENERAL INFORMATION:
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// OTHER INFORMATION: n = A,T,C or G
US-10-027-632-174961
ch 11.9%;
1 Similarity 70.5%;
43; Conservative
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1 Similarity 55.7%;
59; Conservative
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Best Local Similarity
      Query Match
Best Local Similarity
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 174961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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PLICANT: Mary Jame Cunninghan
PLICANT: Marblew R. Kaser
TO INVENTION MARKER GENES RESPONDING TO TREATMENT WITH TOXINS
LE REFERENCE: RA-0039 US
REBRET FILMS DATE: 2001-12-05
MRERET FILMS DATE: 2001-12-05
MRERET FILMS DATE: 2001-12-05
MRERET FILMS DATE: 2011-12-05
MRERET FILMS

nence 506, Application US/10006285 lication No. US20030165854A1 ERAL INFORMATION:

T 12

153 TCATCGGGAGC 163

291 GCATCTGCCGC 281

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106805 GCTTTTCCCCCCCATCACCTCCCACTCTCCATGTGTTCACAAACTAGTCTGGGGCTT 106864
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                                                                                                                                                                                                                                                                                                                                                             106 GATTITICCCATCCTACTITCATCCCGGGCTACAAGGCTICCCAAGCTCATCGGGAGCAA 165
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                                                                                                                                                                                                 DB 13; Length 256525;
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                                                                                                                                                                                           Score 29.6; DB 13; Length
Pred. No. 38;
0; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46; Indels
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Pred. No. 10;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106865 TAGGGCCTAGCATTGTGAAGATGG 106888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166 CAGGATCTATTGTGGTGGAGTCGG 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ERSULT. BESULT. 18
US-09-919-497-18
IS-08-919-497 No. Ng. 192003106662A1
; Parent INFORMATION:
                                     ; LOCATION: (1)...(256525)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-451
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Best Local Similarity 55.3%;
Matches 57; Conservative
                                                                                                                                                                                                 Query Match
Best Local Similarity 59.5%;
Matches 50; Conservative
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , ORGANISM: Homo sapiens
US-09-919-497-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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      351 TCACGTACTTGGGGCCCTCCCGCTTGTAATGCCGGACCACCACGTGCCGTTGT 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93 TARARIACTACGGGATTITICCCATCCTACTTTCATCCCGGGCTACAAGGCTTCCCAAGC 152
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ry Match 11.1%; Score 30.2; DB 15; Length 1759; the Local Similarity 51.3; Prech. No. 3.1; chee 68; Conservative 0; Mismatches 63; Indels 0; Conservative

MERCHAIT MOTTIE, David N.
PLICUAT: MOTTIE, David N.
PLICUAT: MOTTIE, David N.
TLE OF INVERTION: NOTEL COMP.
TLE OF INVERTION: CALCER
ILE REFERENCE: 22945200112 . CALCER
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ILE REFERENCE: 22045200112 . CALCER
ILE REFERENCE: 22045200112 . CALCER
ILE REFERENCE: 2004-00-01.91
RREMY PLILING DATE: 2007-01-01.91
REMARKE: FastSid for Windows Version 4.0
REMARKE: FastSid for Windows Version 4.0
REMARKE: REMSER AND STATES . REMARKE: REMISSID FOR WINDOWS VERSION 4.0

TYPE: DNA
DRGANISM: Mus musculus
FEATURE:

nence 451, Application US/10087192 Mication No. US20020182586A1 MERAL INFORMATION:

AME/KEY: misc_feature THER INFORMATION: Incyte ID No. US20030165854A1 235106.13

YPE: DNA RGANISM: Homo sapiens

AME/KEY: unsure ACATION: 1183-1314, 1485-1577 THER INFORMATION: a, t, c, g, or other --006-288-506

; ORGANISM: Homo sapiens US-09:967-768A-303

Query Match 10.8%; Score 29.4; DB 9; Length 6746; Best Local Similarity 55.3%; Pred. No. 10; Marches 57; Conservative 0; Mismatches 46; Indels 0;

99 IACIACGAGATITITCCCATCCTACTTCATCCCGGGCTACAAGGCTTCCCAAGCTCATC 157
1928 IACIACGAGATTTTCCCTACCTACACCAACTCCAAGAGTTCTGCCTC 1997 0; Gaps

> 8 ò

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Search completed: May 16, 2004, 15:00:17 Job time : 416 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

- nucleic search, using sw model cleic May 16, 2004, 12:37:50 ; Search time 3198 Seconds (withbout alignmenta) 2530.558 Million cell updates/sec

US-09-701-023-2 ct score:

1 gtagcatcgatctctaacaa......tactcatgagctctctca 271

IDENTITY NUC Gapop 10.0 , Gapext 1.0

ng table:

55026578 27513289 seqs, 14931090276 residues :peq:

. number of hits satisfying chosen parameters:

num DB seq length: 0 num DB seq length: 200000000

Listing first 45 summaries processing: Minimum Match 0% Maximum Match 100%

ase:

EST: *

em_gss_inv:* em_gss_pln:* em_gss_vrt:* em dss hum:* em_gas_mus:* em_gss_fun:* em_gss_mam:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. em gss pro: *
em gss rod: *
em gss pbg: *
em gss vrl: *
gb gss: *

SUMMARIES

BH472044 BOHUA43TR BZ471957 BONNK77TR AZ923008 OSAC4-1 P CG409294 D8990 D8 Description BH472044 BZ471957 AZ923008 CG409294 9 228 Query Match Length DB 641 554 214 282 20.6 20.4 14.8 Score 55.8 55.4 40.2

NACL07 NACL07 NACL06	CG734690 ZMMBBD029 CG171886 PUFMF37TD CG171885 PUFMF37TB CC371520 PUFMF37TB		CC371523 PUHBZ30TD CG873669 ZMMBBC028 CG420254 ZMMBBC003		CG322358 CG08S14TV CD972576 OAE23e03. CC026132 3591 1 CC666071 CGWHR64TH	CG737340 ZMMBBb032 CG435797 OG5DO35TC CC350259 OGPAF79TV		BB442449 BB442449 BZ665884 SGT1742-3 CG738843 ZMMBBC018 BB779656 fZmb014f0 CD974521 OAR&T7b09.	2344 1811 5778 5778 5778 555 58337 8439
CF3313 CF3304 CF3304					29 CG322358 14 CD972576 28 CC026132 29 CC666071			BB44244 BZ66588 CG73884 BH77965	411749114
392 393 601	934 931 991	494 650 667	837 927 972	767 516 279	789 458 501 579	611 699 954	355 576 959 970 911	259 4 4 7 6 4 2 2 2 4 4 3 4 4 4 4 4 4 4 4 4 4 4 4 4	659 710 276 497 603
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ALIGNMENTS

GSS 13-DEC-2001 BOHUA43TR BOHU Brassica oleracea genomic clone BOHUA43, genomic rapi 301.488-3233
Exex. 101.488-3229
Baali: ddtowsEdigr.org
Baali: main ddtowsEdigr.org
Sag Primer: TR
Cates From a doubled haploid provided by Tom Osborn.
Cates inheared ends. 9712 Medical Center Drive, Rockville, MD 20850, USA linear 641 bp BH472044.1 GI:17680155 Contact: Chris Town TIGR Brassica oleracea survey sequence. BH472044 BH472044 VERSION KEYWORDS SOURCE ORGANISM RESULT 1 BH472044/c DEFINITION REFERENCE AUTHORS TITLE JOURNAL COMMENT ACCESSION LOCUS

source

ORIGIN

PRATURES

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214 bp DNA linear GSS 22-WAR-2001
ODAC4-IP CR product directly amplified from genomic DNA Oryza
survey expension cultivar-group) genomic clone 2A-8_A, genomic
survey sequence.
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OUYse astive (aponica cultivar-group)
Bidaryothy Viridijannes; Streptophyra: Embryophyra; Tracheophyra;
Bidaryothyra; Wignolloghyra; Liliopsida; Poales; Poaceae;
Bihhartoidae; Oryseae; Orysa.
I ibases to 214)
Orcoo, K., Owerkerk, P.B.F., Taal, A.J.C., Favalli, C.,
Beggnifisialn'T., Pulsdomenech, P., Colombo, L., Mogs.'J.R.C. and
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Early and multiple Ac transposition in rice suitable for efficient
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                                                                                                                                                                                                            Oryza setiva (japonica cultivar-group)
Oryza setiva (japonica cultivar-group)
Staryophyta; Viridiplantas; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnollophyta, Liliopsida; Poales; Poaceae;
Birnarcideae; Oryzaez; Oryza.
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Pred. No. 0.056;
0; Mismatches 18; Indels 0;
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Plant Mol. Biol. (2001) In press
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Best Local Similarity 73.9%;
Matches 51; Conservative (
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DNN is from a doubled haploid provided by Tom Osborn.
Sag primer: T ends
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                                                                                                                                                  /organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
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/mol_type="genomic DNA"
/strain="TO1000DH3"
                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:3712"
/clone="BOHUA43"
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Fax: 301-838-0208
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DEFINITION

RESULT 2 BZ471957

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SOURCE

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EST 18-AUG-2003
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//dw ebige='proliferated callue on 2N6 media for 30 days"
//dw bose="t.ooli bullone.
//db.hose='s.coli bullone.
//dlone.ilb='Rice callus plasmid CDNA library (NACL)"
//dlone.ilb='Rice callus plasmid CDNA library (NACL)"
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//dlone.ilb='Rice callus plasmid CDNA library (NACL)"
//dlone.ilb='Rice callus plasmid CDNA library (NACL)"
//dlone.ilb-'Rice call
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          391 AGGGATGAAAACGGTCGGTAACGGTCGCTAAAATACCTCTACCGTTTTCATTTTTCATATT 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa
Oryza sativa
Shekrycta, Viridiplantas, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Marchilophyta, Liliopsida, Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genotics and Generics Institute, GreenGene Blotech Inc.; Division of Elecenters and Solutionmeatics, Myongol University Yordin, Nyongol, Korea Bloom and Solutionmeatics, Myongol University Fel: 87 1310 6135
Fel: 82 11 321 6135
Bmail: blankmengablo.com. blankmeblo.myongji.ac.kr. iooseticn/Qealifeters
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/clone_lib="Rice callus plasmid cDNA library (NACL)"
//note=Vector: pCR4-TOPO; Site 1: EcoRi; mRNA was capped
with oligoribonuclectides and then used as templates for
RP-PCR."
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1. thases 1 to 393)
Kim,J.S., Jun,K.M., Cheong P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
arge-each sequencing Analysis of Rice ESTs
(Dipplialsed (200)
                                                                                                                                                                                                                                                                                                                                                                                                                            65 AGGGATGAAAACGGTCGGTCGGTAAAATACTACGGGATTTTTCCCATCCTACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NACL--07-G19.b1 Rice callus plasmid cDNa library (NACL) Oryza sativa cDNa clone NACL--07-G19, mRNA sequence.
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                                                                                                                                                                                                                                                                                Score 39; DB 14; Length 392;
Pred. No. 0.16;
0; Mismatches 15; Indels
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/clone="NACL--07-G19"
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/cultivar="Nackdong"
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Matches 48; Conserv
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CF331337
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                                                       Kim, C.W., Pásón H.L., Park, S.J., Chon, N.S., Je, B.I., Sun, B.,
Park, S.H., Park, J.Y., 4ee, B.J., Kim, M.J., Lee, J.J., Nam, M.H.,
Bun, W.Y. and Han, C.D.
Rapid, Jarge-scale generation of De transposant lines and analysis
of De Local in rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 AGGGATGAAAACGGTCGGTAACGGTCGGTAAAATACCTCTACCGTTTTCATATT 208
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//dev_stage="proliferated callus on 2N6 media for 30 days"
//ab host="E.coll DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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NACL-07-G19.g1 Rice callus plasmid CDNA library (NACL) Oryza sativa cDNA clone NACL-07-G19, mXNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39; DB 29; Length 282;
Pred. No. 0.15;
0; Mismatches 15; Indels
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Location/Qualifiers
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/cultivar="Dongjin"
/db_xref="taxon:39947"
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/clone="NACL--07-G19"
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/cultivar="Nackdong"
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1 Similarity 76.2%;
48; Conservative
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1. Usessel to 93 wather and the American Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel School Company of Markel C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="DH10B"
/Clone libe="MamBab"
/Clone libe="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII; Zea mays L. ssp. mays"
                            University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.0%; Score 38; DB 29; Length 746; 75.8%; Pred. No. 0.42; tive 0; Mismatches 15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'organism="Zea mays subsp. mays"
                                                                                          85721-0088, USA
Fai: 520 626 3967
Fas: 520 621 9288
Email: http://genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/cultivar="B73"
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/strain="B73"
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/db xref="taxon:4578"
/clone="ZMMBBb0290B02"
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Location/Qualifiers
Arizona Genomics Institute
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Other_GSSs: PUFMF37TB
Contact: Cathy Whitelaw
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Class: BAC ends.
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FORWARD: T7
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Zea mays
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E. 1. (Dases I to 601.

S. Kim, J.S., Juh, K.M., Chenga, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S. I., Kim, J.K., Kim, Y.K., Kan, Y.K., and Nahm, B.H.
Large-scale Sequencing Analysis of Rice RSTs
Unpublished (2003)

Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Biosinformatics, Myong31 University
Vonelin, Kyocoggi, Acrea
Peris, 23, 1316 6335

Faxt. 27, 1316 6335
                                                         CF330495

MEAL-06-D19.b1 Rice callus plasmid CDNA library (NACL) Organ RACI-06-D18 clone NACL-06-D19, mRNA sequence.
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Ebikaryote Vitidipiantes Erreptophyta; Embryophyta; Tracheophyta;
Ebikaryote Vitidipiantes Erreptophyta; Embryophyta; Tracheophyta;
Clade; Penicoldees; Paccas, Andropogomese; Zea.
Theses I to 746;
Andropogomese; Zea.
Andropogomese; Zea.
Andropogomese; Zea.
Andropogomese; Zea.
Andropogomese; Zea.
Andropogomese; Zea.
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/lab_host="E.coli DH10B"
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//mote=Vector: pCR4-TOPO; Site 1: EccR1; mRWA was capped
with oligoribonucleotides and then used as templates for
RR-PCR.
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Location/Qualifiers
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/cultivar="Nackdong"
/db_xref="taxon:4530"
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/tissue_type="callus"
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SGT751-3-3 Arabidopsis thaliana baineatrion linear GSS 03-FEB-2003 SGT751-3-3 Arabidopsis thaliana baineation linea Arabidopsis thaliana genomic clone SGT751, genomic survey sequence. BESEGGS BESEGGS CS 01:2819G895
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Plant Cell 11 (12), 2263-2270 (1999)
                                                         CC371520 109 bp DNA linear GSS 19-MAY-2003 PHDE3GTB ZM_0.6_1.0 KB Zea mays genomic clone ZMWBT416F12, genomic eurvey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158 AGGGATGAAAACGGTCGGGAACGGTCGCTAAAATACCTCTACCGTTTTCATTTTCATATT 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enkaryota, Viridiplantas, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Maynollophyta, endicotyledons, core eudicots; core eudicots; core eudicots; core eudicots; coredas envoalda II. Brassicales, Brassicaceae, Arabidopsis. 1 (bases 1 to 494) Parinov, S., Serugan, M., De, Y., Yang, W.C., Kumaran, M. and Sindaresan, V.
                                                                                                                                                                                                                                                                                                                                   Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Lilopaida, Poales, Poaceae, PNCCAD
Clada, Panicoideae, Andropogonae, Zea.
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/At.51.#873."
/Ab.xef="axxd:4577"
/Alone="wwwBnaiderl2"
/Alone="weeler to Wa" x=750; Site_1: EcoRI; 0.6-1.0 kb high
Or selected genomic_DNA.lbxary"
                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 309)
Whitelaw,C.A., Onackenbush,J., Van Aken,S., Utterback,T.,
Resnick,P. Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bennetzen,J.
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1. Similarity 74.6%; Pred. No. 0.5; 17. Conservative 0; Mismatches 16; Indels 0; Mismatches 16; Indels 0;
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Arabidopsis thaliana
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Unpublished (2003)
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Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Other GSSs: PUHBZ30TD
Contact: Cathy Whitelaw
                                                                                                                                                                                                           CC371520.1 GI:30845137
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Best Local Similarity
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AUTHORS
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COMMENT
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     RESULT 11
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Spenatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
Clade, Panicoideae, Andropogonae, Zea.
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
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                                                                                                                                                                                                                                     Length 934;
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Fred. No. 0.62;
                                                                                                                                                                                                                                     Score 37.6; DB 29;
Pred. No. 0.6;
0; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 AATACTACGGGATTTTTCCCATCCTACTTTCA 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              776 AATACCTCTACCGTTTTCATTTTAA 807
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/mol_type="genomic DNA"
/strain="B73"
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Unpublished (2003)
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Email: whitelaw@tigr.org
Seg primer: TR
Class: sheared ends.
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Contact: Cathy Whitelaw
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CG171885.1 GI:34062683
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at Local Similarity 63.0%;
ches 58; Conservative
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                                                                                                                                                                                               65 AGGGATGAAAACGGTCGGTAACGGTCGGTAAAATACTACGGGATTTTTCCCATCCTACTT 124
                                                                                                                                                                                                                                                         550 AGGGATGAAAACGGTCGGGAACGGTCGGTAAAATACCTCTACCGTTTTCATTTTCATATT 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 AGGGATGAAAACGGTCGGTAACGGTCGGTAAAATACTACGGGATTTTTCCCATCCTACTT 124
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Spematophyta, Magnoliophyta; Lilopsida; Poales; Poaceae; PRCCAD
Slade; Panicoldeae; Andropogomee; Zea.
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Whitelaw.C.A., Quackenbuh.J., Van Aken.S., Utterback.T.,
Remitck., Framer.C.M., Budhman.M., Bedell,J.A., Rohlfing.T.,
Citek. N., Numberg.A., Robbins.D. and Lakey.N.
Consortium for Maize Genomics
                                                                                                                               Gaps
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/clone lib="xk 0,7 1.5 KB"
/clone="Vector: pBCSk-7 Site 1: HincII; 0,7-1.5 kb
methylation filered genomic DNA library"
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                                                                    Length 650;
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                                                                                                                               16; Indels
                                                                    DB 14;
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                                                               13.8%; Score 37.4; DB 74.6%; Pred. No. 0.63; ive 0, Mismatches
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/strain="B73"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genomic survey sequence.
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Other GSSs: OGWHP66TH
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Fax: 301-838-0208
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traingoene from the line SGT75. Some insertion lines may have more traingoene from the line SGT75. Some insertion lines may have more historic one Desent, but > 50-5% of the lines contain single insertions or linestions carry a reporter GUS gene as a gene trap. The line from which the sequence was obtained is available from the Arabidopsis Biological Resource Center (ARRC), stock number CR0354. This line can be ordered from the Arabidopsis line can be ordered from the Arabidopsis lines on the Arabidopsis lines are also the Sesurce (ARRC) and the Sesurce (ARRC) are also the service of the Sesurce (ARRC) are also the service of the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurce (ARRC) are also the Sesurc
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Sprancophyta; Kagnoliophyta; Lilopsida; Poales; Poaceae; PACLAO
Slado; Panicoldae, Andropogonae; Zea.
Contact: Sundaresan V
University of California at Davis
Life Sciences Addition 1002, University of California, Davis CA
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Dr. Joachim Messings alab
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Fax: 732-445-5735
Email: jlai@waksma
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Brkerycta; Viridiplantae; Streptophyta; Enbryophyta; Tracheophyta;
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